

STN SEARCH HISTORY

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 15:42:52 ON 29 AUG 2006

L1 26928 SEA PPARGAMMA OR (PPAR(A) GAMMA) OR (PERIXISOME PROLIFERATOR-AC
TIVATED RECEPTOR) OR MPPAR OR PPARALPHA OR (PPAR(A) ALPHA) OR
(THIAZOLIDINEDIONE RECEPTOR) OR PPAR

L2 15785 SEA (SERUM AMYLOID A) OR (AMYLOID A) OR SAA1 OR SAA OR
(AMYLOID PROTEIN A)

L3 64619 SEA (COX(A) 2) OR COXII OR COX-2 OR COX2 OR (CYCLO-OXYGENASE(A)
II) OR (CYCLOOXYGENASE(A) 2) OR CYCLOOXYGENASE2 OR PTGS2 OR
PGHS-2 OR (PROTAGLANDIN H SYNTHASE-2)

L4 66070 SEA IL-8 OR IL8 OR (INTERLEUKIN(A) 8) OR (INTERLEUKIN(A) VIII)
OR INTERLEUKIN-8 OR (LEUKOCYTE ADHESION INHIBITOR)

L5 2 SEA L1 AND L2 AND L3 AND L4

L6 1 DUP REM L5 (1 DUPLICATE REMOVED)

L7 0 SEA L6 AND PY<2004
D L6,BIB,1

L8 17 SEA L4 AND L3 AND L2

L9 13 DUP REM L8 (4 DUPLICATES REMOVED)

L10 5 SEA L9 AND PY<2004
D L10,BIB,1-4
D L10,BIB,5
D L10,ABS,5
D L10,ABS,2

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1573	(serum adj amyloid adj a adj protein) or (amyloid adj a) or SAA1 or (amyloid adj protein adj a)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 15:13
L2	3816	PPARGgamma or (PPAR adj gamma) or (peroxisome adj proliferator-Activated adj receptor) or (perixisome adj proliferator adj activated adj receptor) or (PPAR adj alpha) or PPARAlpha or mPPARGgamma or (thiazolidinedione adj receptor)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 15:13
L3	4938	PPARGgamma or (PPAR adj gamma) or (peroxisome adj proliferator-Activated adj receptor) or (perixisome adj proliferator adj activated adj receptor) or (PPAR adj alpha) or PPARAlpha or mPPARGgamma or (thiazolidinedione adj receptor) or PPAR	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 15:13
L4	3124	(serum adj amyloid adj a adj protein) or (amyloid adj a) or SAA1 or (amyloid adj protein adj a) or SAA	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 16:20
L5	8252	(COX adj 2) or COX-2 or COX2 or (cyclo-oxygenase adj II) or (cyclooxygenase-2) or PTGS2 or PGHS-2 or (prostaglandin adj H adj synthase-2)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 16:21
L6	12342	IL-8 or (IL adj "8") or IL8 or (interleukin adj "8") or interleukin-8 or (leukocyte adj adhesion adj inhibitor)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 16:22
L7	19	L3 and L4 and I5 and L6	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 15:33
L8	8	L7 and ((colorectal or colon\$4 or rectal or rectum) with (cancer or polyp or neoplasia or tumor or tumour or adenoma\$4))	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 16:25
L9	36985	435/6.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 15:33

EAST Search History

L10	461	L9 and L3	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 15:34
L11	24	L10 and L4	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 15:34
L12	9	L11 and L5	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 15:34
L13	3	L12 and L6	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 16:20
L14	11660	435/7.1.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 16:20
L15	45084	L14 or L9	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 16:20
L16	12475	(serum amyloid A protein) or (amyloid adj a) or SAA1 or (amyloid protein A) or SAA	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 16:21
L17	8318	(COX adj 2) or COX-2 or COX2 or (cyclo-oxygenase adj II) or (cyclooxygenase-2) or PTGS2 or PGHS-2 or (prostaglandin H synthase-2)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 16:21
L18	20575	IL-8 or (IL adj "8") or IL8 or (interleukin adj "8") or interleukin-8 or (leukocyte adhesion inhibitor)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 16:23
L19	379	L16 and L17 and L18	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 16:23
L20	73	L19 and L9	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 16:25
L21	45	L20 and ((colorectal or colon\$4 or rectal or rectum) with (cancer or polyp or neoplasia or tumor or tumour or adenoma\$4))	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 16:29

EAST Search History

L22	16	L21 and (PPARgamma or PPARalpha or PPAR)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/29 16:29
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SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-53.rnj.

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OM nucleic - nucleic search, using sw model

```
Run on:      July 13, 2006, 01:59:35 ; Search time 115.116 Seconds
              (without alignments)
              357.590 Million cell updates/sec
```

Title: US-10-690-880-53
Perfect score: 22
Sequence: 1 gggacatgtggagagcctactc 22

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size : 25

Total number of hits satisfying chosen parameters: 0

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Listing first 45 summaries

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Database :      Issued_Patents_NA:*
1:   /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2:   /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3:   /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4:   /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5:   /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6:   /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7:   /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8:   /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9:   /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10:  /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query						
No.	Score	Match	Length	DB	ID				Description

No matches found

Search completed: July 13, 2006, 02:48:02
Job time : 115.116 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-5.rge.

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 05:16:01 ; Search time 2028.35 Seconds
(without alignments)
11633.404 Million cell updates/sec

Title: US-10-690-880-5
Perfect score: 369
Sequence: 1 atgaagcttctcacgggcct.....gcctgcctgagaaatactga 369

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	369	100.0	369	5	HUMAMYSA1A	M23698 Homo sapien
2	369	100.0	610	5	BC105796	BC105796 Homo sapi
3	369	100.0	663	2	BD028341	BD028341 Sequence
4	369	100.0	663	2	AR728602	AR728602 Sequence
5	369	100.0	663	2	AX892808	AX892808 Sequence
6	368.6	100.0	516	2	BD027481	BD027481 Sequence
7	368.6	100.0	516	2	AR727742	AR727742 Sequence
8	368.6	100.0	516	2	AX887871	AX887871 Sequence
9	367.4	99.6	369	5	HUMSAAM	M10906 Human serum
10	365.8	99.1	722	2	CS081991	CS081991 Sequence
11	364.6	98.8	523	7	BV168205	BV168205 sqnm7682
12	364.6	98.8	652	7	BV180637	BV180637 sqnm11060
13	364.2	98.7	369	2	CQ714757	CQ714757 Sequence
14	364.2	98.7	537	5	BC007022	BC007022 Homo sapi
15	362.8	98.3	366	5	CR542241	CR542241 Homo sapi
16	362.8	98.3	369	8	AY893946	AY893946 Synthetic
17	349.8	94.8	369	2	CQ725149	CQ725149 Sequence
18	349.8	94.8	369	2	AX774864	AX774864 Sequence
19	349.8	94.8	369	5	HUMAMYSA2A	M23699 Homo sapien
20	349.8	94.8	526	2	BD091193	BD091193 P53-induc
21	349.8	94.8	526	2	AR223017	AR223017 Sequence
22	349.8	94.8	526	5	HUMSAAB	M26152 Homo sapien
23	349.8	94.8	570	5	BC020795	BC020795 Homo sapi
24	348.2	94.4	369	5	HUMAMYSA2B	M23700 Homo sapien
25	344.2	93.3	575	2	BD034654	BD034654 Sequence
26	344.2	93.3	575	2	AR734915	AR734915 Sequence
27	344.2	93.3	575	2	AX899121	AX899121 Sequence
28	340.8	92.4	499	5	HSSAAS8	X51445 Human mRNA
29	297.8	80.7	1471	2	CS071176	CS071176 Sequence
30	294.4	79.8	386	2	CQ518027	CQ518027 Sequence
31	268.2	72.7	569	14	S71722	S71722 serum amylo
32	263.4	71.4	513	14	S71725	S71725 serum amylo
33	263.4	71.4	548	14	OCAMYAR	X16428 Rabbit mRNA
34	258.6	70.1	510	14	OCLSPMRNA	X58728 O.cuniculus
35	247	66.9	402	2	CQ920520	CQ920520 Sequence
36	245.8	66.6	471	14	RABSAA3	M64696 Rabbit seru
37	241	65.3	248	2	CS070968	CS070968 Sequence
38	234.6	63.6	429	6	BC024606	BC024606 Mus muscu
39	234.6	63.6	642	2	CS211138	CS211138 Sequence
40	234.6	63.6	642	2	CS214780	CS214780 Sequence
41	233	63.1	637	6	BC087933	BC087933 Mus muscu
42	231.4	62.7	530	6	HAMSAA3A	M33431 M.auratus s
43	231.4	62.7	576	6	MMU60438	U60438 Mus musculu
44	231.4	62.7	607	6	MUSSAA2A	M11130 Mouse serum
45	231	62.6	393	14	DQ367410	DQ367410 Sus scrof

ALIGNMENTS

RESULT 1
HUMAMYSA1A

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 06:25:38 ; Search time 42.3305 Seconds
(without alignments)
12153.869 Million cell updates/sec

Title: US-10-690-880-5
Perfect score: 369
Sequence: 1 atgaagcttctcacgggcct.....gcctgcctgagaaatactga 369

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 886355 seqs, 697127050 residues

Total number of hits satisfying chosen parameters: 1772710

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
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2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	369	100.0	369	8 US-11-242-111-16	Sequence 16, Appl

2	369	100.0	369	8	US-11-006-161-1	Sequence 1, Appli
3	367.4	99.6	535	8	US-11-266-748A-228612	Sequence 228612,
4	367.4	99.6	535	8	US-11-266-748A-363010	Sequence 363010,
c 5	367.4	99.6	535	8	US-11-266-748A-446389	Sequence 446389,
6	367.4	99.6	689	8	US-11-266-748A-87251	Sequence 87251, A
7	367.4	99.6	689	8	US-11-266-748A-112354	Sequence 112354,
c 8	367.4	99.6	689	8	US-11-266-748A-140062	Sequence 140062,
9	364.2	98.7	622	8	US-11-266-748A-177459	Sequence 177459,
10	349.8	94.8	369	8	US-11-006-161-8	Sequence 8, Appli
11	349.8	94.8	526	8	US-11-266-748A-402579	Sequence 402579,
c 12	349.8	94.8	526	8	US-11-266-748A-473625	Sequence 473625,
13	349.8	94.8	570	8	US-11-006-161-3	Sequence 3, Appli
14	349.8	94.8	903	8	US-11-266-748A-87250	Sequence 87250, A
15	349.8	94.8	903	8	US-11-266-748A-112353	Sequence 112353,
c 16	349.8	94.8	903	8	US-11-266-748A-140061	Sequence 140061,
17	348.2	94.4	369	8	US-11-006-161-10	Sequence 10, Appl
18	282	76.4	336	6	US-10-501-187-276	Sequence 276, App
19	223.6	60.6	762	8	US-11-266-748A-20644	Sequence 20644, A
20	186.4	50.5	193	8	US-11-006-161-6	Sequence 6, Appli
21	184.6	50.0	492	8	US-11-266-748A-217356	Sequence 217356,
22	178.2	48.3	614	8	US-11-266-748A-287377	Sequence 287377,
c 23	178.2	48.3	614	8	US-11-266-748A-338806	Sequence 338806,
24	178.2	48.3	745	8	US-11-266-748A-218916	Sequence 218916,
25	166.6	45.1	655	8	US-11-266-748A-391176	Sequence 391176,
c 26	166.6	45.1	655	8	US-11-266-748A-481894	Sequence 481894,
27	108.4	29.4	1000	8	US-11-266-748A-282387	Sequence 282387,
c 28	108.4	29.4	1000	8	US-11-266-748A-309027	Sequence 309027,
29	108.4	29.4	4286	8	US-11-006-161-5	Sequence 5, Appli
30	63.8	17.3	1000	8	US-11-266-748A-390364	Sequence 390364,
c 31	63.8	17.3	1000	8	US-11-266-748A-481082	Sequence 481082,
32	33	8.9	1435	7	US-11-305-666-25	Sequence 25, Appl
33	32.6	8.8	2355	6	US-10-449-902-28015	Sequence 28015, A
34	32.2	8.7	5251	7	US-11-218-305-451	Sequence 451, App
35	32	8.7	1507	8	US-11-266-748A-188013	Sequence 188013,
36	32	8.7	1754	8	US-11-266-748A-188014	Sequence 188014,
37	32	8.7	1754	8	US-11-266-748A-194551	Sequence 194551,
38	32	8.7	2533	8	US-11-266-748A-27267	Sequence 27267, A
39	32	8.7	2547	8	US-11-266-748A-24334	Sequence 24334, A
40	31.6	8.6	355	8	US-11-266-748A-378061	Sequence 378061,
c 41	31.6	8.6	355	8	US-11-266-748A-461440	Sequence 461440,
42	31.6	8.6	5493	6	US-10-517-441-86	Sequence 86, Appl
43	31.2	8.5	921	7	US-11-056-355B-12809	Sequence 12809, A
44	31.2	8.5	1004	7	US-11-218-305-12908	Sequence 12908, A
45	31.2	8.5	1710	7	US-11-218-305-5036	Sequence 5036, Ap

ALIGNMENTS

RESULT 1

US-11-242-111-16

; Sequence 16, Application US/11242111

; Publication No. US20060088862A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Nancy M

; TITLE OF INVENTION: DRUG SCREENING AND MOLECULAR DIAGNOSTIC TEST FOR EARLY DETECTIO

; TITLE OF INVENTION: OF COLORECTAL CANCER: REAGENTS, METHODS, AND KITS THEREOF

; FILE REFERENCE: NLEE-01001US1 MCF/MLB

; CURRENT APPLICATION NUMBER: US/11/242,111

; CURRENT FILING DATE: 2005-09-29

; PRIOR APPLICATION NUMBER: 60/614,746

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 06:23:19 ; Search time 410.786 Seconds
(without alignments)
11037.706 Million cell updates/sec

Title: US-10-690-880-5
Perfect score: 369
Sequence: 1 atgaagcttctcacgggcct.....gcctgcctgagaaatactga 369

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	369	100.0	369	6	US-10-205-823-354	Sequence 354, App
2	369	100.0	369	9	US-10-690-880-5	Sequence 5, Appli
3	369	100.0	369	13	US-11-005-923-1	Sequence 1, Appli
4	369	100.0	369	13	US-11-006-007-1	Sequence 1, Appli
5	369	100.0	369	13	US-11-000-757-1	Sequence 1, Appli
6	369	100.0	369	13	US-11-051-454-354	Sequence 354, App
7	369	100.0	516	3	US-09-974-298-27	Sequence 27, Appl
c 8	367.4	99.6	559	9	US-10-723-860-2384	Sequence 2384, Ap
9	367.4	99.6	661	3	US-09-974-298-26	Sequence 26, Appl
10	367.4	99.6	1067	6	US-10-198-846-13386	Sequence 13386, A
11	365.8	99.1	414	3	US-09-918-995-8699	Sequence 8699, Ap
12	365.8	99.1	722	16	US-11-177-506-21	Sequence 21, Appl
13	365.8	99.1	764	9	US-10-481-652-7	Sequence 7, Appli
14	352.2	95.4	754	9	US-10-481-652-8	Sequence 8, Appli
15	349.8	94.8	369	7	US-10-101-510-329	Sequence 329, App
16	349.8	94.8	369	8	US-10-283-975A-180	Sequence 180, App
17	349.8	94.8	369	10	US-10-849-989-33	Sequence 33, Appl
18	349.8	94.8	369	13	US-11-005-923-8	Sequence 8, Appli
19	349.8	94.8	369	13	US-11-006-007-8	Sequence 8, Appli
20	349.8	94.8	369	13	US-11-000-757-8	Sequence 8, Appli
21	349.8	94.8	398	3	US-09-918-995-8123	Sequence 8123, Ap
22	349.8	94.8	526	3	US-09-154-750A-71	Sequence 71, Appl
23	349.8	94.8	570	13	US-11-005-923-3	Sequence 3, Appli
24	349.8	94.8	570	13	US-11-006-007-3	Sequence 3, Appli
25	349.8	94.8	570	13	US-11-000-757-3	Sequence 3, Appli
26	349.8	94.8	955	9	US-10-723-860-6571	Sequence 6571, Ap
27	348.2	94.4	369	13	US-11-005-923-10	Sequence 10, Appl
28	348.2	94.4	369	13	US-11-006-007-10	Sequence 10, Appl
29	348.2	94.4	369	13	US-11-000-757-10	Sequence 10, Appl
30	341.2	92.5	755	9	US-10-481-652-5	Sequence 5, Appli
31	294.4	79.8	386	9	US-10-357-930-49894	Sequence 49894, A
32	234.6	63.6	642	16	US-11-128-061-457	Sequence 457, App
33	234.6	63.6	642	16	US-11-128-061-4099	Sequence 4099, Ap
34	234.6	63.6	642	16	US-11-128-049-457	Sequence 457, App
35	234.6	63.6	642	16	US-11-128-049-4099	Sequence 4099, Ap
36	229.8	62.3	369	13	US-11-014-625-3	Sequence 3, Appli
c 37	229.8	62.3	369	13	US-11-014-625-6	Sequence 6, Appli
38	228.2	61.8	606	3	US-09-917-800A-1390	Sequence 1390, Ap
c 39	222.6	60.3	907	9	US-10-481-652-11	Sequence 11, Appl
c 40	215.8	58.5	655	16	US-11-136-527-1280	Sequence 1280, Ap
41	215.8	58.5	655	16	US-11-136-527-5376	Sequence 5376, Ap
42	200.8	54.4	396	7	US-10-116-788A-12	Sequence 12, Appl
43	200.8	54.4	396	11	US-10-116-788A-12	Sequence 12, Appl
44	186.4	50.5	193	13	US-11-005-923-6	Sequence 6, Appli
45	186.4	50.5	193	13	US-11-006-007-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-10-205-823-354

; Sequence 354, Application US/10205823

; Publication No. US20030108963A1

; GENERAL INFORMATION:

Result No.	Score	% Match	Query Length	DB	ID	Description
1	369	100.0	663	3	US-09-513-999C-8671	Sequence 8671, Ap
2	368.6	100.0	516	3	US-09-513-999C-3734	Sequence 3734, Ap
3	364.2	98.7	369	3	US-09-949-016-5383	Sequence 5383, Ap
4	349.8	94.8	369	3	US-09-949-016-4040	Sequence 4040, Ap
5	349.8	94.8	526	3	US-09-154-750A-71	Sequence 71, Appl
6	344.2	93.3	575	3	US-09-513-999C-14984	Sequence 14984, A
7	218.2	59.1	317	3	US-09-621-976-17490	Sequence 17490, A
8	178.2	48.3	614	3	US-09-920-672-3	Sequence 3, Appli
9	178.2	48.3	614	3	US-09-949-016-860	Sequence 860, App
10	178.2	48.3	614	3	US-09-949-016-5386	Sequence 5386, Ap
11	178.2	48.3	614	4	US-09-880-107-2404	Sequence 2404, Ap
12	178.2	48.3	624	3	US-09-919-039-7	Sequence 7, Appli
13	142	38.5	6913	3	US-09-949-016-17125	Sequence 17125, A
14	136.8	37.1	6635	3	US-09-949-016-15782	Sequence 15782, A
15	108.6	29.4	232	3	US-09-513-999C-13854	Sequence 13854, A
16	103.8	28.1	277	3	US-09-513-999C-8539	Sequence 8539, Ap
17	90.4	24.5	5847	3	US-09-920-672-10	Sequence 10, Appl
18	90.4	24.5	9447	3	US-09-949-016-12602	Sequence 12602, A
19	90.4	24.5	9447	3	US-09-949-016-17128	Sequence 17128, A
20	87	23.6	87	3	US-10-045-360-4	Sequence 4, Appli
21	80.6	21.8	87	3	US-10-045-360-6	Sequence 6, Appli
22	63.8	17.3	456	3	US-09-920-672-11	Sequence 11, Appl
23	63.8	17.3	456	4	US-09-880-107-3017	Sequence 3017, Ap
c 24	63.8	17.3	601	3	US-09-949-016-34695	Sequence 34695, A
c 25	63.8	17.3	601	3	US-09-949-016-188266	Sequence 188266,
c 26	51.8	14.0	375	4	US-09-880-107-2452	Sequence 2452, Ap
c 27	41.2	11.2	7218	2	US-08-232-463-14	Sequence 14, Appl
c 28	33.4	9.1	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 29	33.4	9.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 30	32.4	8.8	4318	3	US-09-949-016-1583	Sequence 1583, Ap
c 31	32.4	8.8	17879	3	US-09-949-016-13325	Sequence 13325, A
32	32	8.7	1794	3	US-09-902-540-8754	Sequence 8754, Ap
33	32	8.7	2072	3	US-09-774-528-107	Sequence 107, App
34	32	8.7	2072	3	US-10-120-988-107	Sequence 107, App
35	32	8.7	2440	3	US-09-774-528-106	Sequence 106, App
36	32	8.7	2440	3	US-10-120-988-106	Sequence 106, App
37	32	8.7	9556	3	US-09-902-540-929	Sequence 929, App
c 38	31.6	8.6	98962	3	US-09-949-016-14133	Sequence 14133, A
c 39	31.6	8.6	102884	3	US-09-949-016-17100	Sequence 17100, A
c 40	30.6	8.3	954	3	US-09-418-641-3	Sequence 3, Appli
c 41	30.6	8.3	285478	3	US-09-949-016-13362	Sequence 13362, A
42	30.4	8.2	324	3	US-09-533-559-1615	Sequence 1615, Ap
c 43	30.4	8.2	601	3	US-09-949-016-141514	Sequence 141514,
c 44	30.4	8.2	601	3	US-09-949-016-156791	Sequence 156791,
c 45	30.4	8.2	601	3	US-09-949-016-156792	Sequence 156792,

ALIGNMENTS

RESULT 1

US-09-513-999C-8671
; Sequence 8671, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880- 5.rng.

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 05:02:23 ; Search time 206.503 Seconds
(without alignments)
12458.724 Million cell updates/sec

Title: US-10-690-880-5
Perfect score: 369
Sequence: 1 atgaagcttctcacgggcct.....gcctgcctgagaaatactga 369

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	369	100.0	369	10	ADB75530	Adb75530 Prostate
2	369	100.0	369	12	ADL26821	Adl26821 Human ser
3	369	100.0	369	12	ADN05778	Adn05778 Antipsori
4	369	100.0	369	14	ADW72107	Adw72107 Human SAA
5	369	100.0	369	14	AEA60824	Aea60824 Human ser
6	369	100.0	369	14	AEA55219	Aea55219 Human ser
7	369	100.0	369	14	AEB09894	Aeb09894 Human DNA
8	369	100.0	516	8	ABX77525	Abx77525 Different
9	369	100.0	663	3	AAC04596	Aac04596 Human sec
10	368.6	100.0	516	3	AAC03736	Aac03736 Human sec
c 11	367.4	99.6	559	6	ABT10099	Abt10099 Human bre
c 12	367.4	99.6	559	12	ADQ19565	Adq19565 Human sof
c 13	367.4	99.6	559	15	AEF74606	Aef74606 Human pol
14	367.4	99.6	661	8	ABX77524	Abx77524 Different
15	367.4	99.6	1067	11	ACN92236	Acn92236 Breast ca
16	365.8	99.1	414	9	ACH21487	Ach21487 Human adu
17	365.8	99.1	722	14	ADZ75612	Adz75612 Human ser
18	365.8	99.1	722	15	AEE39870	Aee39870 Amyloid A
19	365.8	99.1	722	15	AEF39166	Aef39166 DNA encod
20	365.8	99.1	764	10	ACC48065	Acc48065 Nucleotid
21	358.4	97.1	471	14	ACL54328	Acl54328 Human col
22	352.2	95.4	754	10	ACC48066	Acc48066 Nucleotid
23	349.8	94.8	369	6	ABZ35217	Abz35217 Human gen
24	349.8	94.8	369	10	ADE84961	Ade84961 Farnesyl
25	349.8	94.8	369	14	ADZ21677	Adz21677 Serum amy
26	349.8	94.8	369	14	AEA60831	Aea60831 Human ser
27	349.8	94.8	369	14	AEA55226	Aea55226 Human ser
28	349.8	94.8	369	14	AEB09901	Aeb09901 Human DNA
29	349.8	94.8	398	9	ACH20911	Ach20911 Human adu
30	349.8	94.8	526	2	AAX86268	Aax86268 DNA encod
31	349.8	94.8	526	12	ADN04671	Adn04671 Antipsori
32	349.8	94.8	526	15	AEF96632	Aef96632 Colorecta
33	349.8	94.8	548	10	ABZ84561	Abz84561 Toxicolog
34	349.8	94.8	570	14	AEA60826	Aea60826 Human ser
35	349.8	94.8	570	14	AEA55221	Aea55221 Human ser
36	349.8	94.8	570	14	AEB09896	Aeb09896 Human DNA
37	349.8	94.8	955	12	ADQ23751	Adq23751 Human sof
38	348.2	94.4	369	14	AEA60833	Aea60833 Human ser
39	348.2	94.4	369	14	AEA55228	Aea55228 Human ser
40	348.2	94.4	369	14	AEB09903	Aeb09903 Human DNA
41	344.2	93.3	575	3	AAC10909	Aac10909 Human sec
42	341.2	92.5	541	14	ACL54429	Acl54429 Human col
43	341.2	92.5	755	10	ACC48063	Acc48063 Nucleotid
44	297.8	80.7	1471	4	AAH57499	Aah57499 Human liv
45	294.4	79.8	386	5	ABV49875	Abv49875 Human pro

ALIGNMENTS

RESULT 1
ADB75530

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OM nucleic - nucleic search, using sw model

```
Run on:      July 13, 2006, 01:58:05 ; Search time 1798.19 Seconds
              (without alignments)
              653.050 Million cell updates/sec
```

```
Title:          US-10-690-880-54
Perfect score:  21
Sequence:       1 catcatagttcccccgagcat 21
```

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size : 25

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

```
Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

No matches found

Search completed: July 13, 2006, 11:17:11
Job time : 1798.19 secs

SCORE 1.3 BuildDate: 12/06/2005

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 02:09:43 ; Search time 63 Seconds
(without alignments)
464.751 Million cell updates/sec

Title: US-10-690-880-54
Perfect score: 21
Sequence: 1 catcatagttcccccgagcat 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 886355 seqs, 697127050 residues

Word size : 25

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					
No.	Score	Match	Length	DB	ID	Description

No matches found

Search completed: July 13, 2006, 02:47:09
Job time : 63 secs

SCORE 1.3 BuildDate: 12/06/2005

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

No matches found

Search completed: July 13, 2006, 03:24:45
Job time : 644.651 secs

SCORE 1.3 BuildDate: 12/06/2005

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 01:59:35 ; Search time 109.884 Seconds
(without alignments)
357.590 Million cell updates/sec

Title: US-10-690-880-54
Perfect score: 21
Sequence: 1 catcatagttcccccgagcat 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size : 25

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%									
Result		Query									
No.	Score	Match	Length	DB	ID	Description					

No matches found

Search completed: July 13, 2006, 02:48:02

Job time : 110.884 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-54.rng.

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 01:44:35 ; Search time 369.698 Seconds
(without alignments)
396.046 Million cell updates/sec

Title: US-10-690-880-54
Perfect score: 21
Sequence: 1 catcatagttcccccgagcat 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 25

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

No matches found

Search completed: July 13, 2006, 03:12:44
Job time : 369.698 secs

SCORE 1.3 BuildDate: 12/06/2005

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http://es/ScoreAccessWeb/GetItem.action?AppId=10690880&seqId=561578&ItemName=... 8/29/2006

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

No matches found

Search completed: July 13, 2006, 02:44:04
Job time : 1304.93 secs

SCORE 1.3 BuildDate: 12/06/2005

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

No matches found

Search completed: July 13, 2006, 11:17:11
Job time : 1883.81 secs

SCORE 1.3 BuildDate: 12/06/2005

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 02:09:43 ; Search time 66 Seconds
(without alignments)
464.751 Million cell updates/sec

Title: US-10-690-880-53
Perfect score: 22
Sequence: 1 gggacatgtggagagcctactc 22

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 886355 seqs, 697127050 residues

Word size : 25

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result		Query				Description	
No.	Score	Match	Length	DB	ID		

No matches found							

Search completed: July 13, 2006, 02:47:09
Job time : 66 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-53.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 02:06:09 ; Search time 675.349 Seconds
(without alignments)
400.279 Million cell updates/sec

Title: US-10-690-880-53
Perfect score: 22
Sequence: 1 gggacatgtggagagcctactc 22

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 18892170 seqs, 6143817638 residues

Word size : 25

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Match	Length	DB	ID	Description	

No matches found

Search completed: July 13, 2006, 03:24:45
Job time : 675.349 secs

SCORE 1.3 BuildDate: 12/06/2005

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 01:44:35 ; Search time 387.302 Seconds
(without alignments)
396.046 Million cell updates/sec

Title: US-10-690-880-53
Perfect score: 22
Sequence: 1 gggacatgtggagagcctactc 22

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 25

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: .geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

No matches found

Search completed: July 13, 2006, 03:12:44
Job time : 387.302 secs

SCORE 1.3 BuildDate: 12/06/2005

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 01:57:25 ; Search time 1367.07 Seconds
(without alignments)
1029.094 Million cell updates/sec

Title: US-10-690-880-53
Perfect score: 22
Sequence: 1 gggacatgtggagagcctactc 22

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size : 25

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_env:*
- 2: gb_pat:*
- 3: gb_ph:*
- 4: gb_pl:*
- 5: gb_pr:*
- 6: gb_ro:*
- 7: gb_sts:*
- 8: gb_sy:*
- 9: gb_un:*
- 10: gb_vi:*
- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

No matches found

Search completed: July 13, 2006, 02:44:04
Job time : 1367.07 secs

SCORE 1.3 BuildDate: 12/06/2005

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http://es/ScoreAccessWeb/GetItem.action?AppId=10690880&seqId=561571&ItemName=... 8/29/2006

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	369	100.0	490	2	BG565032	BG565032 602583825
2	369	100.0	497	7	BF126546	BF126546 601650791
3	369	100.0	497	7	BF126653	BF126653 601650929
4	369	100.0	517	2	BG568516	BG568516 602587493
5	369	100.0	523	5	CD512583	CD512583 AGENCOURT
6	369	100.0	525	4	CB999100	CB999100 AGENCOURT
7	369	100.0	544	2	BG566553	BG566553 602585580
8	369	100.0	547	2	BG568393	BG568393 602587839
9	369	100.0	548	2	BG565915	BG565915 602583083
10	369	100.0	550	2	BG565023	BG565023 602583811
11	369	100.0	550	2	BG568300	BG568300 602587225
12	369	100.0	551	2	BG564258	BG564258 602586055
13	369	100.0	554	2	BG563473	BG563473 602582562
14	369	100.0	554	2	BG567514	BG567514 602586251
15	369	100.0	555	2	BG565718	BG565718 602589051
16	369	100.0	555	2	BG618892	BG618892 602646287
17	369	100.0	556	2	BG616738	BG616738 602614959
18	369	100.0	559	2	BG617518	BG617518 602615191
19	369	100.0	560	2	BG569358	BG569358 602588669
20	369	100.0	566	2	BG568909	BG568909 602588084
21	369	100.0	567	2	BG563505	BG563505 602581901
22	369	100.0	569	2	BG566385	BG566385 602585376
23	369	100.0	569	2	BG618566	BG618566 602645479
24	369	100.0	585	2	BG562539	BG562539 602581590
25	369	100.0	592	2	BG565078	BG565078 602583883
26	369	100.0	613	2	BG566837	BG566837 602589525
27	369	100.0	618	2	BG569266	BG569266 602588556
28	369	100.0	660	2	BG568037	BG568037 602586913
29	369	100.0	702	2	BG565095	BG565095 602583715
30	369	100.0	708	2	BG618863	BG618863 602646254
31	369	100.0	710	2	BG564863	BG564863 602589812
32	369	100.0	754	2	BG567826	BG567826 602586637
33	369	100.0	769	2	BG563257	BG563257 602582183
34	369	100.0	796	2	BG568816	BG568816 602588174
35	369	100.0	798	2	BG566163	BG566163 602582794
36	369	100.0	801	2	BG567754	BG567754 602586553
37	369	100.0	804	2	BG563213	BG563213 602582132
38	369	100.0	805	2	BG562764	BG562764 602581278
39	369	100.0	812	2	BG566282	BG566282 602585151
40	369	100.0	816	2	BG562456	BG562456 602581090
41	369	100.0	823	2	BG618508	BG618508 602645406
42	369	100.0	827	4	CB957394	CB957394 AGENCOURT
43	369	100.0	829	2	BG563632	BG563632 602582377
44	369	100.0	833	2	BG617729	BG617729 602645242
45	369	100.0	835	2	BG568948	BG568948 602587946

ALIGNMENTS

RESULT 1
BG565032
LOCUS

BG565032

490 bp

mRNA

linear

EST 10-APR-2001

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 05:54:59 ; Search time 16507.7 Seconds
(without alignments)
11368.329 Million cell updates/sec

Title: US-10-690-880-2
Perfect score: 3356
Sequence: 1 gtccaggaactcctcagcag.....agctcctcttaagaagatta 3356

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1597.4	47.6	4107	6	AK144726	AK144726 Mus muscu
2	1594.2	47.5	3776	6	AK144956	AK144956 Mus muscu
3	1588.4	47.3	3168	6	AK172161	AK172161 Mus muscu
4	1573.4	46.9	3883	6	AK149820	AK149820 Mus muscu
5	1475	44.0	2565	6	AK166221	AK166221 Mus muscu
6	1442	43.0	2247	6	AK049923	AK049923 Mus muscu
7	973.8	29.0	1037	4	BX363285	BX363285 BX363285
8	887.4	26.4	938	1	AL583668	AL583668 AL583668
9	816.4	24.3	968	4	BX370552	BX370552 BX370552
c 10	748	22.3	810	1	AI971172	AI971172 wr26a04.x
11	731	21.8	762	9	DN995052	DN995052 TC119565
c 12	723.4	21.6	744	5	CD365731	CD365731 UI-H-FT2-
13	715.6	21.3	2132	4	CD014050	CD014050 90138391
14	713	21.2	2003	6	AK170664	AK170664 Mus muscu
15	713	21.2	2306	6	AK134163	AK134163 Mus muscu
16	713	21.2	2319	6	AK138432	AK138432 Mus muscu
17	713	21.2	2323	6	AK170414	AK170414 Mus muscu
18	713	21.2	2353	6	AK142741	AK142741 Mus muscu
19	713	21.2	2355	6	AK163609	AK163609 Mus muscu
20	713	21.2	2793	6	AK046457	AK046457 Mus muscu
21	713	21.2	2865	6	AK159907	AK159907 Mus muscu
22	705.6	21.0	2742	6	AK167357	AK167357 Mus muscu
23	704.4	21.0	818	5	CJ450300	CJ450300 CJ450300
24	704.4	21.0	866	8	CN158532	CN158532 947332 MA
c 25	704.4	21.0	869	8	CN160452	CN160452 949636 MA
26	701.6	20.9	820	5	CD609928	CD609928 56096194H
27	698.8	20.8	2788	6	AK160886	AK160886 Mus muscu
c 28	698	20.8	745	5	CD609930	CD609930 56096286H
29	696.4	20.8	834	10	DV923981	DV923981 LB02932.C
c 30	692.2	20.6	707	4	CA309056	CA309056 UI-H-FT1-
31	687	20.5	808	4	CB960307	CB960307 AGENCOURT
32	686.4	20.5	757	5	CD609931	CD609931 56096286J
33	677.4	20.2	701	1	AL710848	AL710848 DKFZp686N
34	667	19.9	667	8	CN337322	CN337322 170006000
35	662	19.7	662	1	AL710813	AL710813 DKFZp686J
36	660	19.7	1473	14	AY415140	AY415140 Homo sapi
37	654	19.5	1448	14	AY415141	AY415141 Pan trogl
38	642	19.1	1448	14	AY415142	AY415142 Mus muscu
39	640.2	19.1	776	7	AV756509	AV756509 AV756509
c 40	630.6	18.8	663	2	BG055155	BG055155 nad02e05.
c 41	624.6	18.6	631	7	BE673090	BE673090 7d29b11.x
42	620.2	18.5	830	10	DV914214	DV914214 LB02829.C
c 43	614.8	18.3	627	5	CD609929	CD609929 56096194J
44	600.6	17.9	1922	6	CNS0GS1G	CR732367 Tetraodon
45	595.8	17.8	1766	4	CD014048	CD014048 90138112

ALIGNMENTS

RESULT 1

AK144726

LOCUS

AK144726

4107 bp

mRNA

linear

HTC 21-SEP-2005

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 06:25:38 ; Search time 384.99 Seconds
(without alignments)
12153.869 Million cell updates/sec

Title: US-10-690-880-2
Perfect score: 3356
Sequence: 1 gtccaggaactcctcagcag.....agctcctcttaagaagatta 3356

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 886355 seqs, 697127050 residues

Total number of hits satisfying chosen parameters: 1772710

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	3356	100.0	3356	8	US-11-242-111-2	Sequence 2, Appli
2	3343.2	99.6	4465	6	US-10-505-928-528	Sequence 528, App
3	3343.2	99.6	4465	6	US-10-511-937-460	Sequence 460, App
4	3343.2	99.6	4465	8	US-11-266-748A-29135	Sequence 29135, A
5	1621.6	48.3	3509	7	US-11-372-770-4	Sequence 4, Appli
c 6	1621.6	48.3	3509	7	US-11-372-770-6	Sequence 6, Appli
7	1475	44.0	1812	7	US-11-372-770-7	Sequence 7, Appli
c 8	1475	44.0	1812	7	US-11-372-770-8	Sequence 8, Appli
9	723.8	21.6	2539	8	US-11-242-111-15	Sequence 15, Appl
10	703.6	21.0	1899	7	US-11-372-770-15	Sequence 15, Appl
c 11	703.6	21.0	1899	7	US-11-372-770-16	Sequence 16, Appl
12	703.6	21.0	2693	7	US-11-372-770-12	Sequence 12, Appl
c 13	703.6	21.0	2693	7	US-11-372-770-14	Sequence 14, Appl
14	563.8	16.8	4982	8	US-11-266-748A-56408	Sequence 56408, A
15	553.6	16.5	571	8	US-11-266-748A-40271	Sequence 40271, A
c 16	486.8	14.5	1440	8	US-11-266-748A-366061	Sequence 366061,
17	486.8	14.5	1440	8	US-11-266-748A-449440	Sequence 449440,
18	424.2	12.6	542	7	US-11-372-770-1	Sequence 1, Appli
c 19	424.2	12.6	542	7	US-11-372-770-3	Sequence 3, Appli
c 20	374.4	11.2	562	8	US-11-266-748A-163885	Sequence 163885,
21	374.4	11.2	562	8	US-11-266-748A-243855	Sequence 243855,
22	263.4	7.8	1043	8	US-11-266-748A-98137	Sequence 98137, A
c 23	263.4	7.8	1043	8	US-11-266-748A-150948	Sequence 150948,
24	188	5.6	1274	8	US-11-266-748A-83412	Sequence 83412, A
c 25	188	5.6	1274	8	US-11-266-748A-136223	Sequence 136223,
26	160.4	4.8	26782	8	US-11-266-748A-23753	Sequence 23753, A
27	149	4.4	2987	6	US-10-517-441-50	Sequence 50, Appl
28	123	3.7	275	7	US-11-372-770-9	Sequence 9, Appli
c 29	123	3.7	275	7	US-11-372-770-11	Sequence 11, Appl
30	122	3.6	602	8	US-11-301-554-1564	Sequence 1564, Ap
c 31	114.6	3.4	732	8	US-11-266-748A-380552	Sequence 380552,
32	114.6	3.4	732	8	US-11-266-748A-463931	Sequence 463931,
c 33	114.6	3.4	2987	6	US-10-517-441-346	Sequence 346, App
c 34	89.6	2.7	2987	6	US-10-517-441-620	Sequence 620, App
35	76.8	2.3	1184	8	US-11-266-748A-85890	Sequence 85890, A
c 36	76.8	2.3	1184	8	US-11-266-748A-138701	Sequence 138701,
c 37	67.4	2.0	5286	6	US-10-517-441-294	Sequence 294, App
c 38	67.4	2.0	5286	6	US-10-517-441-568	Sequence 568, App
39	64.2	1.9	2987	6	US-10-517-441-345	Sequence 345, App
40	61.4	1.8	19634	6	US-10-517-441-413	Sequence 413, App
41	61.4	1.8	19634	6	US-10-517-441-687	Sequence 687, App
42	55.6	1.7	5286	6	US-10-517-441-294	Sequence 294, App
43	55.6	1.7	5286	6	US-10-517-441-568	Sequence 568, App
44	54.2	1.6	16579	6	US-10-517-441-290	Sequence 290, App
45	54.2	1.6	16579	6	US-10-517-441-564	Sequence 564, App

ALIGNMENTS

RESULT 1

US-11-242-111-2

; Sequence 2, Application US/11242111

; Publication No. US20060088862A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Nancy M

; TITLE OF INVENTION: DRUG SCREENING AND MOLECULAR DIAGNOSTIC TEST FOR EARLY DETECTIO

; TITLE OF INVENTION: OF COLORECTAL CANCER: REAGENTS, METHODS, AND KITS THEREOF

; FILE REFERENCE: NLEE-01001US1 MCF/MLB

; CURRENT APPLICATION NUMBER: US/11/242,111

; CURRENT FILING DATE: 2005-09-29

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-2.rnpbm.

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Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10690880 and Search Result us-10-690-880-2.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 06:23:19 ; Search time 3736.04 Seconds
(without alignments)
11037.706 Million cell updates/sec

Title: US-10-690-880-2
Perfect score: 3356
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3356	100.0	3356	9	US-10-690-880-2	Sequence 2, Appli
2	3354.4	99.9	4496	6	US-10-044-090-478	Sequence 478, App
3	3354.4	99.9	4496	6	US-10-071-766-46	Sequence 46, Appl
4	3354.4	99.9	4750	7	US-10-247-671-126	Sequence 126, App
5	3343.2	99.6	4465	3	US-09-953-067A-2	Sequence 2, Appli
6	3343.2	99.6	4465	7	US-10-021-660-42	Sequence 42, Appl
7	3343.2	99.6	4465	7	US-10-170-385-238	Sequence 238, App
8	3343.2	99.6	4465	7	US-10-295-027-31	Sequence 31, Appl
9	3343.2	99.6	4465	7	US-10-373-801-11	Sequence 11, Appl
10	3343.2	99.6	4465	8	US-10-211-462-132	Sequence 132, App
11	3343.2	99.6	4465	10	US-10-663-377-25	Sequence 25, Appl
12	3343.2	99.6	4465	15	US-11-000-688-191	Sequence 191, App
13	3205.8	95.5	3387	6	US-10-027-961A-19	Sequence 19, Appl
14	3204.2	95.5	3387	7	US-10-191-997-87	Sequence 87, Appl
15	3204.2	95.5	3387	8	US-10-641-643-1050	Sequence 1050, Ap
16	3204.2	95.5	3387	9	US-10-278-698-136	Sequence 136, App
17	3204.2	95.5	3387	9	US-10-278-698-652	Sequence 652, App
18	2536.6	75.6	2563	6	US-10-044-090-477	Sequence 477, App
19	1856.8	55.3	11064	3	US-09-949-293-25	Sequence 25, Appl
20	1850.4	55.1	9453	3	US-09-954-456-324	Sequence 324, App
21	1850.4	55.1	9453	8	US-10-717-597-209	Sequence 209, App
22	1850.4	55.1	9453	10	US-10-843-641A-3351	Sequence 3351, Ap
23	1850.4	55.1	9453	10	US-10-505-680-482	Sequence 482, App
24	1808	53.9	1834	8	US-10-308-920-3	Sequence 3, Appli
25	1808	53.9	1834	8	US-10-308-920-14	Sequence 14, Appl
26	1621.6	48.3	3509	3	US-09-919-060-4	Sequence 4, Appli
c 27	1621.6	48.3	3509	3	US-09-919-060-6	Sequence 6, Appli
28	1621.6	48.3	3509	8	US-10-679-140-4	Sequence 4, Appli
c 29	1621.6	48.3	3509	8	US-10-679-140-6	Sequence 6, Appli
30	1609.6	48.0	3489	8	US-10-315-218-11	Sequence 11, Appl
31	1576.8	47.0	3986	3	US-09-953-067A-6	Sequence 6, Appli
32	1475	44.0	1812	3	US-09-919-060-7	Sequence 7, Appli
c 33	1475	44.0	1812	3	US-09-919-060-8	Sequence 8, Appli
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c 35	1475	44.0	1812	8	US-10-679-140-8	Sequence 8, Appli
36	1454.2	43.3	4403	16	US-11-136-527-2391	Sequence 2391, Ap
37	1433.6	42.7	4154	8	US-10-664-705-1	Sequence 1, Appli
38	1433.6	42.7	4404	8	US-10-191-803-103	Sequence 103, App
39	1428.2	42.6	2951	8	US-10-264-839-15	Sequence 15, Appl
40	1384.6	41.3	1920	8	US-10-308-920-1	Sequence 1, Appli
41	725.4	21.6	1819	8	US-10-308-920-6	Sequence 6, Appli
42	724.4	21.6	1807	8	US-10-382-248-5	Sequence 5, Appli
43	724.4	21.6	1894	7	US-10-260-937-13	Sequence 13, Appl
44	724.4	21.6	2435	9	US-10-278-698-133	Sequence 133, App
45	724.4	21.6	2435	9	US-10-278-698-649	Sequence 649, App

ALIGNMENTS

RESULT 1

Comments /
Suggestions

start

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OM nucleic - nucleic search, using sw model

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Run on:      July 13, 2006, 05:55:31 ; Search time 611.947 Seconds
              (without alignments)
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Perfect score:  3356
Sequence:       1  gtccaggaactcctcagcag.....agctcctcttaagaaagatta 3356
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Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Post-processing: Minimum Match 0%
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                  Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3205.8	95.5	3387	3	US-08-930-589A-19	Sequence 19, Appl
2	3205.8	95.5	3387	3	US-09-599-781-19	Sequence 19, Appl
3	3205.8	95.5	3387	3	US-10-027-961A-19	Sequence 19, Appl
4	3204.2	95.5	3387	3	US-09-023-655-1050	Sequence 1050, Ap
5	3204.2	95.5	3387	5	US-09-543-679A-2682	Sequence 2682, Ap
6	3204.2	95.5	15240	5	US-09-543-679A-2684	Sequence 2684, Ap
7	3202.6	95.4	3387	2	US-08-064-271-11	Sequence 11, Appl
8	3201	95.4	3387	2	US-08-627-254C-29	Sequence 29, Appl
9	1850.4	55.1	9453	5	US-09-543-679A-2683	Sequence 2683, Ap
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11	1808	53.9	1834	2	US-08-487-753-14	Sequence 14, Appl
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13	1808	53.9	1834	2	US-08-480-065-14	Sequence 14, Appl
14	1808	53.9	1834	3	US-08-487-744-3	Sequence 3, Appli
15	1808	53.9	1834	3	US-08-487-744-14	Sequence 14, Appl
16	1808	53.9	1834	7	PCT-US93-09167-3	Sequence 3, Appli
17	1621.6	48.3	3509	3	US-09-919-060-4	Sequence 4, Appli
c 18	1621.6	48.3	3509	3	US-09-919-060-6	Sequence 6, Appli
19	1576.8	47.0	3986	2	US-08-627-254C-27	Sequence 27, Appl
20	1475	44.0	1812	3	US-09-919-060-7	Sequence 7, Appli
c 21	1475	44.0	1812	3	US-09-919-060-8	Sequence 8, Appli
22	1384.6	41.3	1920	2	US-08-487-753-1	Sequence 1, Appli
23	1384.6	41.3	1920	2	US-08-480-065-1	Sequence 1, Appli
24	1384.6	41.3	1920	3	US-08-487-744-1	Sequence 1, Appli
25	1384.6	41.3	1920	7	PCT-US93-09167-1	Sequence 1, Appli
26	725.4	21.6	1819	2	US-08-487-753-6	Sequence 6, Appli
27	725.4	21.6	1819	2	US-08-480-065-6	Sequence 6, Appli
28	725.4	21.6	1819	3	US-08-487-744-6	Sequence 6, Appli
29	725.4	21.6	1819	7	PCT-US93-09167-6	Sequence 6, Appli
30	724.4	21.6	2539	3	US-09-949-016-3943	Sequence 3943, Ap
31	724.4	21.6	2554	3	US-09-949-016-137	Sequence 137, App
32	711.6	21.2	2554	2	US-08-627-254C-28	Sequence 28, Appl
33	711.4	21.2	2757	2	US-08-627-254C-26	Sequence 26, Appl
34	703.6	21.0	1899	3	US-09-919-060-15	Sequence 15, Appl
c 35	703.6	21.0	1899	3	US-09-919-060-16	Sequence 16, Appl
36	703.6	21.0	2693	3	US-09-919-060-12	Sequence 12, Appl
c 37	703.6	21.0	2693	3	US-09-919-060-14	Sequence 14, Appl
38	653.6	19.5	1920	3	US-08-459-493-2	Sequence 2, Appli
39	428.6	12.8	429	3	US-09-641-638-330	Sequence 330, App
40	428.6	12.8	429	3	US-10-170-097-330	Sequence 330, App
41	424.2	12.6	542	3	US-09-919-060-1	Sequence 1, Appli
c 42	424.2	12.6	542	3	US-09-919-060-3	Sequence 3, Appli
43	395.6	11.8	418	3	US-09-641-638-329	Sequence 329, App
44	395.6	11.8	418	3	US-09-641-638-588	Sequence 588, App
45	395.6	11.8	418	3	US-10-170-097-329	Sequence 329, App

ALIGNMENTS

RESULT 1

US-08-930-589A-19

; Sequence 19, Application US/08930589A

; Patent No. 6107087

; GENERAL INFORMATION:

; APPLICANT: MERCK FROSST CANADA & CO.

; APPLICANT: O'NEILL, GARY P.

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-2.rng.

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 05:02:23 ; Search time 1878.11 Seconds
(without alignments)
12458.724 Million cell updates/sec

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5	3343.2	99.6	4465	6	ABV77992	Abv77992 Hypoxia-r
6	3343.2	99.6	4465	9	ACC57774	Acc57774 Human cyc
7	3343.2	99.6	4465	10	ACF79931	Acf79931 Breast ca
8	3343.2	99.6	4465	10	ABX08805	Abx08805 Angiogene
9	3343.2	99.6	4465	11	ADN38713	Adn38713 Cancer/an
10	3343.2	99.6	4465	11	ADN95605	Adn95605 Human BEC
11	3343.2	99.6	4465	12	ADO24386	Ado24386 Human PRO
12	3343.2	99.6	4465	12	ADP10451	Adp10451 Reference
13	3343.2	99.6	4465	13	ADQ80275	Adq80275 Prostagla
14	3343.2	99.6	4465	13	ADU05832	Adu05832 Novel bro
15	3343.2	99.6	4465	14	ADX85144	Adx85144 Human pro
16	3343.2	99.6	4465	14	ADY15397	Ady15397 DNA encod
17	3343.2	99.6	4465	14	ADY19547	Ady19547 DNA encod
18	3343.2	99.6	4465	14	ADZ59960	Adz59960 Human COX
19	3343.2	99.6	4465	14	AEA23664	Aea23664 Human PRO
20	3343.2	99.6	4465	15	AEF92709	Aef92709 Human COX
21	3340.2	99.5	3373	10	ADL13871	Adl13871 Osteoarth
22	3300.4	98.3	3362	13	ADS87768	Ads87768 Human pro
23	3204.2	95.5	3387	3	AAA34993	Aaa34993 Human ade
24	3204.2	95.5	3387	3	AAF21115	Aaf21115 Human low
25	3204.2	95.5	3387	6	ABA94344	Aba94344 Human cyc
26	3204.2	95.5	3387	10	ABZ96809	Abz96809 Human nuc
27	3204.2	95.5	3387	10	ACF63365	Acf63365 Human cyc
28	3204.2	95.5	3387	10	ADL13868	Adl13868 Osteoarth
29	3204.2	95.5	3387	11	ADI31724	Adi31724 Human cDN
30	3204.2	95.5	3387	11	ABD20658	Abd20658 Human pul
31	3204.2	95.5	3387	13	ADS83791	Ads83791 Human lym
32	3204.2	95.5	3387	14	AED68414	Aed68414 Human COX
33	3204.2	95.5	3387	15	AEF92696	Aef92696 Human mit
34	3204.2	95.5	15240	3	AAA34995	Aaa34995 Human ade
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37	3204.2	95.5	15240	11	ABD20660	Abd20660 Human pul
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39	3199.4	95.3	3387	2	AAQ71002	Aaq71002 Cyclooxyg
40	3098.4	92.3	3266	13	ADS87767	Ads87767 Human pro
41	2536.6	75.6	2563	8	ABX63477	Abx63477 Human cDN
42	1858.4	55.4	11064	9	ADA20274	Ada20274 Human cyc
43	1850.4	55.1	9451	6	ABS97450	Abs97450 Human cyc
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45	1850.4	55.1	9453	6	ABL65014	Abl65014 Lung canc

ALIGNMENTS

RESULT 1
ADW72104

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 05:16:01 ; Search time 18447.5 Seconds
(without alignments)
11633.404 Million cell updates/sec

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Perfect score: 3356
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3354.4	99.9	4465	2	CQ728731	CQ728731 Sequence
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5	3343.2	99.6	4465	2	CS035847	CS035847 Sequence
6	3343.2	99.6	4465	2	CS040649	CS040649 Sequence
7	3343.2	99.6	4465	2	CS044799	CS044799 Sequence
8	3343.2	99.6	4465	2	CS108198	CS108198 Sequence
9	3343.2	99.6	4465	2	CS118144	CS118144 Sequence
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12	3205.8	95.5	3387	2	AR106720	AR106720 Sequence
13	3205.8	95.5	3387	2	AR202531	AR202531 Sequence
14	3205.8	95.5	3387	2	AR473840	AR473840 Sequence
15	3204.2	95.5	3387	2	AR380505	AR380505 Sequence
16	3204.2	95.5	3387	2	AX082878	AX082878 Sequence
17	3204.2	95.5	3387	5	HUMCYCLOX	M90100 Homo sapien
18	3202.6	95.4	3387	2	I24360	I24360 Sequence 11
19	3201	95.4	3387	2	AR029278	AR029278 Sequence
20	3201	95.4	3387	2	AX328834	AX328834 Sequence
21	3098.4	92.3	3266	2	CQ800947	CQ800947 Sequence
22	2912.2	86.8	3669	5	AY151286	AY151286 Homo sapi
23	1962.6	58.5	3314	14	U97696	U97696 Oryctolagus
c 24	1858.4	55.4	84412	5	HS973M2	AL033533 Human DNA
25	1856.8	55.3	11449	5	AY229989	AY229989 Homo sapi
26	1856.8	55.3	12551	5	AY382629	AY382629 Homo sapi
27	1850.4	55.1	9453	2	AX332842	AX332842 Sequence
28	1850.4	55.1	9453	5	HSU04636	U04636 Human cyclo
29	1842.6	54.9	10997	5	HUMPTGS2	D28235 Human PTGS2
30	1815	54.1	1815	5	AY462100	AY462100 Homo sapi
31	1808	53.9	1834	2	AR055229	AR055229 Sequence
32	1808	53.9	1834	2	AR055235	AR055235 Sequence
33	1657.2	49.4	3398	14	AF027334	AF027334 Equus cab
34	1656.8	49.4	3621	14	AY028583	AY028583 Sus scrof
35	1621.6	48.3	3509	2	AR411929	AR411929 Sequence
c 36	1621.6	48.3	3509	2	AR411930	AR411930 Sequence
37	1620	48.3	3632	2	AX082874	AX082874 Sequence
38	1611.4	48.0	1719	2	CQ800945	CQ800945 Sequence
39	1609.6	48.0	3489	14	AF031698	AF031698 Bos tauru
40	1605	47.8	3498	14	AY044905	AY044905 Canis fam
41	1599	47.6	4152	2	AX306255	AX306255 Sequence
42	1599	47.6	4152	6	MUSGRIPGHS	M88242 Mouse gluco
43	1587.4	47.3	3483	14	OAU68486	U68486 Ovis aries
44	1585	47.2	1705	5	AJ634912	AJ634912 Homo sapi
45	1576.8	47.0	3986	2	AR029276	AR029276 Sequence

ALIGNMENTS

RESULT 1
CQ728731

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-16.rst.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
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This page gives you Search Results detail for the Application 10690880 and Search Result us-10-690-880-16.rst.

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 05:54:59 ; Search time 7914.46 Seconds
(without alignments)
11368.329 Million cell updates/sec

Title: US-10-690-880-16
Perfect score: 1609
Sequence: 1 ttcaagtctttttcttttaa.....tctacaaggacttgtactag 1609

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1516.4	94.2	1518	14	AY413103	AY413103 Homo sapi
2	1503.8	93.5	1518	14	AY413104	AY413104 Pan trogl
3	1438	89.4	1722	6	CR599329	CR599329 full-leng
4	1437.4	89.3	1740	6	CR609454	CR609454 full-leng
5	1416.4	88.0	1866	6	CR622226	CR622226 full-leng
6	1403.8	87.2	1828	6	CR857213	CR857213 Pongo pyg
7	1278	79.4	1518	14	AY413105	AY413105 Mus muscu
8	1258	78.2	1402	6	CR609113	CR609113 full-leng
9	1258	78.2	1425	6	CR605352	CR605352 full-leng
10	1013.2	63.0	1116	4	BX424883	BX424883 BX424883
11	874.4	54.3	985	1	AL549611	AL549611 AL549611
12	858	53.3	948	3	BU526666	BU526666 AGENCOURT
c 13	842.6	52.4	1060	1	AL549707	AL549707 AL549707
14	829	51.5	1101	1	AL545177	AL545177 AL545177
15	826	51.3	901	2	BI820841	BI820841 603034063
c 16	802.4	49.9	973	1	AL570116	AL570116 AL570116
17	792.6	49.3	1071	4	BX402494	BX402494 BX402494
c 18	785.2	48.8	1075	4	BX402493	BX402493 BX402493
19	782.8	48.7	1135	4	BX363320	BX363320 BX363320
20	779.8	48.5	944	3	BQ883138	BQ883138 AGENCOURT
21	776.8	48.3	925	1	AL543579	AL543579 AL543579
c 22	774.6	48.1	1073	1	AL523433	AL523433 AL523433
23	774.2	48.1	906	1	AL549037	AL549037 AL549037
24	774.2	48.1	915	4	BX328128	BX328128 BX328128
25	768	47.7	1313	8	CV860288	CV860288 gonad_EST
c 26	754.2	46.9	1072	1	AL571005	AL571005 AL571005
27	751.6	46.7	793	2	BG742110	BG742110 602633578
c 28	750.4	46.6	950	1	AL573383	AL573383 AL573383
29	748.2	46.5	872	3	BQ722874	BQ722874 AGENCOURT
c 30	723.4	45.0	853	8	CR940043	CR940043 CR940043
31	718.2	44.6	861	8	CR939576	CR939576 CR939576
32	712	44.3	854	8	CR940114	CR940114 CR940114
33	702.2	43.6	888	2	BG166774	BG166774 602339105
34	701.6	43.6	813	10	DV816379	DV816379 LB01719.C
35	701.2	43.6	907	10	DV918529	DV918529 LB02913.C
36	701.2	43.6	981	1	AL523434	AL523434 AL523434
37	695.4	43.2	803	8	CR849208	CR849208 CR849208
38	694.6	43.2	938	8	CO579312	CO579312 ILLUMIGEN
39	687.2	42.7	812	8	CR939718	CR939718 CR939718
40	685.4	42.6	839	8	CR939186	CR939186 CR939186
41	682.6	42.4	1088	2	BG179310	BG179310 602331030
42	682.2	42.4	826	7	BE535401	BE535401 601058554
c 43	679.8	42.2	870	8	CR939379	CR939379 CR939379
44	676.4	42.0	980	4	BX363318	BX363318 BX363318
45	671.8	41.8	868	8	CR939958	CR939958 CR939958

ALIGNMENTS

RESULT 1

AY413103

LOCUS

AY413103

1518 bp

DNA

linear

GSS 17-DEC-2003

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-16.rnpbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 06:25:38 ; Search time 184.579 Seconds
(without alignments)
12153.869 Million cell updates/sec

Title: US-10-690-880-16
Perfect score: 1609
Sequence: 1 ttcaagtctttttcttttaa.....tctacaaggacttgtag 1609

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 886355 seqs, 697127050 residues

Total number of hits satisfying chosen parameters: 1772710

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	1609	100.0	1609	8	US-11-242-111-12	Sequence 12, Appl
2	1609	100.0	1854	8	US-11-283-329-23	Sequence 23, Appl
3	1609	100.0	1863	8	US-11-289-781-3	Sequence 3, Appli
4	1438	89.4	1735	6	US-10-505-928-143	Sequence 143, App
5	1438	89.4	1808	8	US-11-266-748A-28881	Sequence 28881, A
6	1437.4	89.3	1767	8	US-11-145-307A-165	Sequence 165, App
7	1437.4	89.3	1767	8	US-11-283-329-25	Sequence 25, Appl
8	1437.4	89.3	1836	8	US-11-283-329-27	Sequence 27, Appl
9	1426	88.6	1734	8	US-11-283-329-21	Sequence 21, Appl
10	1174.4	73.0	1455	8	US-11-266-748A-94271	Sequence 94271, A
c 11	1174.4	73.0	1455	8	US-11-266-748A-147082	Sequence 147082,
12	814.6	50.6	1017	8	US-11-289-656-5	Sequence 5, Appli
13	814.6	50.6	1017	8	US-11-289-781-12	Sequence 12, Appl
14	788	49.0	1000	8	US-11-266-748A-292279	Sequence 292279,
c 15	788	49.0	1000	8	US-11-266-748A-343708	Sequence 343708,
16	788	49.0	1000	8	US-11-266-748A-403930	Sequence 403930,
c 17	788	49.0	1000	8	US-11-266-748A-474976	Sequence 474976,
18	770	47.9	1000	8	US-11-266-748A-286681	Sequence 286681,
c 19	770	47.9	1000	8	US-11-266-748A-338110	Sequence 338110,
c 20	750.4	46.6	950	8	US-11-266-748A-215920	Sequence 215920,
21	750.4	46.6	950	8	US-11-266-748A-237901	Sequence 237901,
22	710.4	44.2	1199	8	US-11-266-748A-8904	Sequence 8904, Ap
23	492	30.6	3301	8	US-11-242-111-13	Sequence 13, Appl
24	492	30.6	3301	8	US-11-266-748A-61023	Sequence 61023, A
25	492	30.6	3301	8	US-11-266-748A-62084	Sequence 62084, A
26	492	30.6	3328	8	US-11-283-329-17	Sequence 17, Appl
27	492	30.6	3328	8	US-11-289-781-5	Sequence 5, Appli
28	485.2	30.2	1850	8	US-11-242-111-11	Sequence 11, Appl
29	485.2	30.2	1850	8	US-11-283-329-15	Sequence 15, Appl
30	485.2	30.2	8129	8	US-11-266-748A-29151	Sequence 29151, A
31	485.2	30.2	8497	8	US-11-266-748A-29152	Sequence 29152, A
32	485.2	30.2	8497	8	US-11-266-748A-56572	Sequence 56572, A
33	485.2	30.2	10049	8	US-11-289-781-1	Sequence 1, Appli
34	451	28.0	148828	8	US-11-266-748A-24893	Sequence 24893, A
35	368.2	22.9	1977	8	US-11-266-748A-25551	Sequence 25551, A
36	366.6	22.8	1977	8	US-11-283-329-19	Sequence 19, Appl
37	359.2	22.3	1089	8	US-11-289-656-9	Sequence 9, Appli
38	359.2	22.3	1089	8	US-11-289-781-16	Sequence 16, Appl
39	351	21.8	634	8	US-11-266-748A-6400	Sequence 6400, Ap
40	347	21.6	1014	8	US-11-289-656-1	Sequence 1, Appli
41	347	21.6	1014	8	US-11-289-781-8	Sequence 8, Appli
42	250	15.5	1000	8	US-11-266-748A-206223	Sequence 206223,
43	250	15.5	1000	8	US-11-266-748A-282714	Sequence 282714,
c 44	250	15.5	1000	8	US-11-266-748A-309354	Sequence 309354,
45	250	15.5	1000	8	US-11-266-748A-392229	Sequence 392229,

ALIGNMENTS

RESULT 1

US-11-242-111-12

; Sequence 12, Application US/11242111

; Publication No. US20060088862A1

GENERAL INFORMATION:

; APPLICANT: Lee, Nancy M

; TITLE OF INVENTION: DRUG SCREENING AND MOLECULAR DIAGNOSTIC TEST FOR EARLY DETECTIO

; TITLE OF INVENTION: OF COLORECTAL CANCER: REAGENTS, METHODS, AND KITS THEREOF

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-16.rnpbm.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 06:23:19.; Search time 1791.21 Seconds
(without alignments)
11037.706 Million cell updates/sec

Title: US-10-690-880-16
Perfect score: 1609
Sequence: 1 ttcaagtctttttcttttaa.....tctacaaggacttgtag 1609

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1609	100.0	1609	9	US-10-690-880-16	Sequence 16, Appl
2	1603.2	99.6	1608	3	US-09-765-111A-15	Sequence 15, Appl
3	1603.2	99.6	1608	10	US-10-181-176-3	Sequence 3, Appli
4	1575.8	97.9	1679	6	US-10-109-886-5	Sequence 5, Appli
5	1518	94.3	1518	7	US-10-414-692-3	Sequence 3, Appli
6	1518	94.3	1518	7	US-10-305-720-1136	Sequence 1136, Ap
7	1518	94.3	1518	10	US-10-502-279-1	Sequence 1, Appli
8	1518	94.3	1518	10	US-10-519-447-3	Sequence 3, Appli
9	1439.2	89.4	2596	3	US-09-765-111A-22	Sequence 22, Appl
10	1439.2	89.4	2625	3	US-09-765-111A-5	Sequence 5, Appli
11	1438	89.4	1808	8	US-10-717-597-99	Sequence 99, Appl
12	1438	89.4	1808	9	US-10-723-860-1495	Sequence 1495, Ap
13	1438	89.4	1835	9	US-10-723-860-5936	Sequence 5936, Ap
14	1438	89.4	2334	3	US-09-765-111A-1	Sequence 1, Appli
15	1438	89.4	2523	3	US-09-765-111A-3	Sequence 3, Appli
16	1437.4	89.3	1757	8	US-10-425-114-28973	Sequence 28973, A
17	1437.4	89.3	1810	6	US-10-116-802-91	Sequence 91, Appl
18	1437.4	89.3	1936	9	US-10-847-732-1	Sequence 1, Appli
19	1437.4	89.3	3389	3	US-09-971-392-96	Sequence 96, Appl
20	1418.6	88.2	1811	3	US-09-765-111A-26	Sequence 26, Appl
21	1418.6	88.2	1811	3	US-09-880-107-2212	Sequence 2212, Ap
c 22	1418.6	88.2	2260	3	US-09-816-828-8	Sequence 8, Appli
c 23	1418.6	88.2	2260	10	US-10-972-024-136	Sequence 136, App
c 24	1418.6	88.2	2295	10	US-10-220-335-78	Sequence 78, Appl
c 25	1418.6	88.2	2307	6	US-10-125-237-5	Sequence 5, Appli
c 26	1418.6	88.2	2307	6	US-10-105-891-5	Sequence 5, Appli
c 27	1418.6	88.2	2307	10	US-10-972-024-5	Sequence 5, Appli
c 28	1418.6	88.2	2329	3	US-09-816-828-9	Sequence 9, Appli
c 29	1418.6	88.2	2329	10	US-10-972-024-137	Sequence 137, App
30	1330.8	82.7	1518	6	US-10-322-332-1	Sequence 1, Appli
31	1292.8	80.3	1790	16	US-11-136-527-2252	Sequence 2252, Ap
32	1222.6	76.0	2005	3	US-09-788-070-1	Sequence 1, Appli
33	1222.6	76.0	2005	6	US-10-142-373-1	Sequence 1, Appli
34	1221	75.9	2130	10	US-10-764-420-212	Sequence 212, App
35	1217.8	75.7	1636	10	US-10-764-420-103	Sequence 103, App
36	1181.4	73.4	1710	16	US-11-128-061-3402	Sequence 3402, Ap
37	1181.4	73.4	1710	16	US-11-128-049-3402	Sequence 3402, Ap
38	941	58.5	1278	6	US-10-106-698-565	Sequence 565, App
39	506.4	31.5	1542	7	US-10-160-807-97	Sequence 97, Appl
40	506.4	31.5	1542	8	US-10-655-847-97	Sequence 97, Appl
41	503.2	31.3	1323	6	US-10-013-807-1	Sequence 1, Appli
42	503.2	31.3	1323	6	US-10-179-403-1	Sequence 1, Appli
43	503.2	31.3	1323	7	US-10-327-813-13	Sequence 13, Appl
44	503.2	31.3	1323	7	US-10-329-668-13	Sequence 13, Appl
45	503.2	31.3	1323	7	US-10-160-807-99	Sequence 99, Appl

ALIGNMENTS

RESULT 1

SCORE Search Results Details for Application 10690880 Search Result us-10-690-880-16.rni.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 05:55:31 ; Search time 293.392 Seconds
(without alignments)
10261.408 Million cell updates/sec

Title: US-10-690-880-16
Perfect score: 1609
Sequence: 1 ttcaagtctttttcttttaa.....tctacaaggacttgtag 1609

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	1607.4	99.9	1812	3	US-09-949-016-3749	Sequence 3749, Ap
2	1607.4	99.9	1812	3	US-09-949-016-3750	Sequence 3750, Ap
3	1603.2	99.6	1608	3	US-09-484-345-3	Sequence 3, Appli
4	1603.2	99.6	1608	3	US-09-765-111A-15	Sequence 15, Appl
5	1575.8	97.9	1679	3	US-09-514-247A-5	Sequence 5, Appli
6	1518	94.3	1518	3	US-09-128-142-3	Sequence 3, Appli
7	1518	94.3	1518	3	US-09-016-434-1136	Sequence 1136, Ap
8	1439.2	89.4	2596	3	US-09-765-111A-22	Sequence 22, Appl
9	1439.2	89.4	2625	3	US-09-765-111A-5	Sequence 5, Appli
10	1438	89.4	1841	3	US-09-587-549C-1	Sequence 1, Appli
11	1438	89.4	2334	3	US-09-765-111A-1	Sequence 1, Appli
12	1438	89.4	2523	3	US-09-765-111A-3	Sequence 3, Appli
13	1434	89.1	1434	3	US-09-128-142-1	Sequence 1, Appli
14	1418.6	88.2	1811	3	US-09-166-265-6	Sequence 6, Appli
15	1418.6	88.2	1811	3	US-09-765-111A-26	Sequence 26, Appl
16	1418.6	88.2	1811	4	US-09-880-107-2212	Sequence 2212, Ap
17	1418.6	88.2	1844	3	US-08-134-557D-1	Sequence 1, Appli
18	1222.6	76.0	1796	3	US-09-255-392-1	Sequence 1, Appli
19	1222.6	76.0	2005	2	US-08-484-200-1	Sequence 1, Appli
20	1222.6	76.0	2005	2	US-08-477-493-1	Sequence 1, Appli
21	1222.6	76.0	2005	3	US-08-465-375-1	Sequence 1, Appli
22	1222.6	76.0	2005	3	US-09-788-070-1	Sequence 1, Appli
23	1222.6	76.0	2005	3	US-10-142-373-1	Sequence 1, Appli
24	1222.6	76.0	2005	3	US-09-155-252A-1	Sequence 1, Appli
25	503.2	31.3	1323	3	US-10-329-668-13	Sequence 13, Appl
26	503.2	31.3	2012	2	US-08-484-200-3	Sequence 3, Appli
27	493.6	30.7	1505	3	US-09-949-016-5726	Sequence 5726, Ap
28	492	30.6	1792	3	US-09-976-594-999	Sequence 999, App
29	492	30.6	3301	3	US-09-166-265-8	Sequence 8, Appli
30	490.4	30.5	2009	2	US-08-333-358-9	Sequence 9, Appli
31	490.4	30.5	2009	2	US-08-463-694-9	Sequence 9, Appli
32	490.4	30.5	2009	2	US-08-694-501-9	Sequence 9, Appli
33	485.2	30.2	1812	3	US-09-949-016-5065	Sequence 5065, Ap
34	485.2	30.2	1850	3	US-09-662-386-1	Sequence 1, Appli
35	485.2	30.2	1854	3	US-09-166-265-4	Sequence 4, Appli
36	482	30.0	2081	3	US-10-329-668-11	Sequence 11, Appl
37	475.6	29.6	1407	2	US-08-459-287-1	Sequence 1, Appli
38	451	28.0	86877	3	US-09-949-016-15491	Sequence 15491, A
39	451	28.0	86877	3	US-09-949-016-15492	Sequence 15492, A
40	292.6	18.2	373	3	US-08-917-653-3	Sequence 3, Appli
41	195	12.1	88906	3	US-09-949-016-17468	Sequence 17468, A
42	194	12.1	87752	3	US-09-949-016-16807	Sequence 16807, A
43	175.6	10.9	277	3	US-08-917-653-4	Sequence 4, Appli
44	173	10.8	1100	3	US-09-484-345-10	Sequence 10, Appl
45	172.6	10.7	601	3	US-09-949-016-133111	Sequence 133111,

ALIGNMENTS

RESULT 1

US-09-949-016-3749

; Sequence 3749, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-16.rng.

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 05:02:23 ; Search time 900.441 Seconds
(without alignments)
12458.724 Million cell updates/sec

Title: US-10-690-880-16
Perfect score: 1609
Sequence: 1 ttcaagtctttttcttttaa.....tctacaaggacttgtag 1609

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1609	100.0	1609	14	ADW72118	Adw72118 Human PPA
2	1609	100.0	1854	13	ADP24099	Adp24099 PRO polyp
3	1609	100.0	1854	15	AEE72157	Aee72157 Human tar
4	1609	100.0	1854	15	AEF96708	Aef96708 Colorecta
5	1605.2	99.8	1848	13	ADS34825	Ads34825 Human aut
6	1604.2	99.7	1647	2	AAT35334	Aat35334 Peroxisom
7	1603.2	99.6	1608	4	AAH76288	Aah76288 Human PPA
8	1603.2	99.6	1608	5	AAF23644	Aaf23644 Human PPA
9	1603.2	99.6	1608	14	AEC31191	Aec31191 Human per
10	1603.2	99.6	1608	14	AED60702	Aed60702 Human per
11	1518	94.3	1518	4	AAD21022	Aad21022 Human per
12	1518	94.3	1518	10	ADB80256	Adb80256 PPARgamma
13	1518	94.3	1518	10	AAD58565	Aad58565 Human PPA
14	1518	94.3	1518	10	ACA56538	Aca56538 Human sig
15	1518	94.3	1518	12	ADI56334	Adi56334 Human pol
16	1518	94.3	1518	12	ADI32750	Adi32750 Human per
17	1518	94.3	1518	12	ADJ92804	Adj92804 Human per
18	1518	94.3	1518	12	ADM31018	Adm31018 Human per
19	1439.2	89.4	2596	4	AAH76294	Aah76294 Human PAX
20	1439.2	89.4	2625	4	AAH76283	Aah76283 Human PAX
21	1438	89.4	1735	11	ADN95221	Adn95221 Human BEC
22	1438	89.4	1735	12	ADO24550	Ado24550 Human PRO
23	1438	89.4	1735	13	ACF87400	Acf87400 Human SIR
24	1438	89.4	1735	14	AEA23975	Aea23975 Human PRO
25	1438	89.4	1735	15	AEE72156	Aee72156 Human tar
26	1438	89.4	1735	15	AEF96710	Aef96710 Colorecta
27	1438	89.4	1766	14	ADV16845	Adv16845 Human per
28	1438	89.4	1808	12	ADP13363	Adp13363 Renal cel
29	1438	89.4	1808	12	ADQ18676	Adq18676 Human sof
30	1438	89.4	1835	12	ADQ23116	Adq23116 Human sof
31	1438	89.4	1841	13	ADT98160	Adt98160 Human per
32	1438	89.4	2334	4	AAH76281	Aah76281 Human PAX
33	1438	89.4	2523	4	AAH76282	Aah76282 Human PAX
34	1437.4	89.3	1757	13	ADX54233	Adx54233 Plant ful
35	1437.4	89.3	1767	15	AEE80877	Aee80877 Human cDN
36	1437.4	89.3	1767	15	AEE72158	Aee72158 Human tar
37	1437.4	89.3	1767	15	AEF96709	Aef96709 Colorecta
38	1437.4	89.3	1810	9	ACH03886	Ach03886 Human cDN
39	1437.4	89.3	1836	15	AEE72159	Aee72159 Human tar
40	1437.4	89.3	1836	15	AEF96613	Aef96613 Colorecta
41	1437.4	89.3	1936	2	AAT35333	Aat35333 Peroxisom
42	1437.4	89.3	3389	10	ADB47396	Adb47396 Human cDN
43	1434.6	89.2	1751	13	ADS34827	Ads34827 Human aut
44	1434	89.1	1434	4	AAD21021	Aad21021 Human per
45	1428	88.8	1428	12	ADP05750	Adp05750 Human nuc

ALIGNMENTS

RESULT 1
ADW72118

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Suggestions

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http://es/ScoreAccessWeb/GetItem.action?AppId=10690880&seqId=561554&ItemName=... 8/29/2006

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1609	100.0	1854	2	CS246469	CS246469 Sequence
2	1607.4	99.9	1609	2	CQ723688	CQ723688 Sequence
3	1605.2	99.8	1848	2	CQ925006	CQ925006 Sequence
4	1603.2	99.6	1608	2	AR121467	AR121467 Sequence
5	1603.2	99.6	1608	2	CS186182	CS186182 Sequence
6	1603.2	99.6	1608	2	AR526811	AR526811 Sequence
7	1603.2	99.6	1608	5	HSU79012	U79012 Human ligand
8	1575.8	97.9	1679	2	AR203332	AR203332 Sequence
9	1575.8	97.9	1679	5	HUMPPARG	D83233 Homo sapien
10	1518	94.3	1518	2	AR270573	AR270573 Sequence
11	1518	94.3	1518	5	HSU63415	U63415 Human perox
12	1506.8	93.6	1759	5	AF033103	AF033103 Macaca mu
13	1502	93.3	1765	5	AY048695	AY048695 Macaca fa
14	1439.2	89.4	2596	2	AR526817	AR526817 Sequence
15	1439.2	89.4	2625	2	AR526806	AR526806 Sequence
16	1438	89.4	1642	2	CQ723687	CQ723687 Sequence
17	1438	89.4	1735	2	CS108509	CS108509 Sequence
18	1438	89.4	1735	2	CS246468	CS246468 Sequence
19	1438	89.4	1766	5	HSPPARGAM	X90563 H.sapiens m
20	1438	89.4	1808	5	HUMPPARGB	L40904 Homo sapien
21	1438	89.4	1841	2	AR594814	AR594814 Sequence
22	1438	89.4	2334	2	AR526804	AR526804 Sequence
23	1438	89.4	2523	2	AR526805	AR526805 Sequence
24	1437.4	89.3	1755	5	AY222643	AY222643 Homo sapi
25	1437.4	89.3	1767	2	CS246470	CS246470 Sequence
26	1437.4	89.3	1767	2	CS254021	CS254021 Sequence
27	1437.4	89.3	1767	5	BC006811	BC006811 Homo sapi
28	1437.4	89.3	1836	2	CS246471	CS246471 Sequence
29	1436.4	89.3	1473	5	AK223528	AK223528 Homo sapi
30	1434.6	89.2	1751	2	CQ925008	CQ925008 Sequence
31	1434	89.1	1434	5	BT007281	BT007281 Homo sapi
32	1434	89.1	1434	8	AY889210	AY889210 Synthetic
33	1428	88.8	1428	8	AY890395	AY890395 Synthetic
34	1428	88.8	1428	8	AY893460	AY893460 Synthetic
35	1426.4	88.7	1428	8	AY892864	AY892864 Synthetic
36	1426.4	88.7	1428	8	AY893907	AY893907 Synthetic
37	1418.6	88.2	1811	2	AR473660	AR473660 Sequence
38	1418.6	88.2	1811	2	AR526819	AR526819 Sequence
39	1418.6	88.2	1811	2	AX409565	AX409565 Sequence
40	1418.6	88.2	1844	2	AR139020	AR139020 Sequence
c 41	1418.6	88.2	2260	2	CS185653	CS185653 Sequence
c 42	1418.6	88.2	2307	2	CS185522	CS185522 Sequence
c 43	1418.6	88.2	2329	2	CS185654	CS185654 Sequence
44	1406.4	87.4	1849	5	AY048698	AY048698 Macaca fa
45	1400.8	87.1	1766	5	AF033343	AF033343 Macaca mu

ALIGNMENTS

RESULT 1
CS246469

Comments /
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start

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OM nucleic - nucleic search, using sw model

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Run on:      July 13, 2006, 05:16:01 ; Search time 8954.42 Seconds
              (without alignments)
              11633.404 Million cell updates/sec
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Title: US-10-690-880-1
Perfect score: 1629
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

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Database :                               GenEmbl:*
1:      gb_env:*
2:      gb_pat:*
3:      gb_ph:*
4:      gb_pl:*
5:      gb_pr:*
6:      gb_ro:*
7:      gb_sts:*
8:      gb_sy:*
9:      gb_un:*
10:     gb_vi:*
11:     gb_ov:*
12:     gb_htg:*
13:     gb_in:*
14:     gb_om:*
15:     gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1594	97.9	1633	2	AR762925	AR762925 Sequence
2	1594	97.9	1666	2	CQ959822	CQ959822 Sequence
3	1594	97.9	1666	2	CS031231	CS031231 Sequence
4	1594	97.9	1666	2	CS035791	CS035791 Sequence
5	1594	97.9	1666	2	CS040183	CS040183 Sequence
6	1594	97.9	1666	2	CS044743	CS044743 Sequence
7	1592.4	97.8	1640	5	AK131067	AK131067 Homo sapi
8	1580.4	97.0	1639	2	AR035066	AR035066 Sequence
9	1580.4	97.0	1639	2	CQ831704	CQ831704 Sequence
10	1580.4	97.0	1639	2	AR264563	AR264563 Sequence
11	1580.4	97.0	1639	2	AX774859	AX774859 Sequence
12	1580.4	97.0	1639	5	HUMBTLP	M17017 Human beta-
13	1569.4	96.3	1639	2	BD094086	BD094086 Shear str
14	1569.4	96.3	1639	2	CQ833971	CQ833971 Sequence
15	1569.4	96.3	1639	2	CQ973498	CQ973498 Sequence
16	1569.4	96.3	1639	2	CS108176	CS108176 Sequence
17	1569.4	96.3	1639	2	CS108200	CS108200 Sequence
18	1569.4	96.3	1639	2	DD174222	DD174222 METHODS O
19	1569.4	96.3	1639	5	HUMMONAP	M26383 Human monoc
20	1561	95.8	1605	5	BC013615	BC013615 Homo sapi
21	1480.8	90.9	1560	2	BD080550	BD080550 Chemokine
22	1480.8	90.9	1560	2	AR242974	AR242974 Sequence
23	1480.8	90.9	1560	2	AR270777	AR270777 Sequence
24	1480.8	90.9	1560	2	AR274938	AR274938 Sequence
25	1480.8	90.9	1560	2	AR368778	AR368778 Sequence
26	1480.8	90.9	1560	5	HSMDNCF	Y00787 Human mRNA
27	1263.2	77.5	7156	5	AF385628	AF385628 Homo sapi
28	1263.2	77.5	78409	5	AC112518	AC112518 Homo sapi
c 29	1263.2	77.5	215102	12	CNS01DW3	AL136327 Homo sapi
30	1260	77.3	154723	12	CNS01DU2	AL133124 Homo sapi
31	1234	75.8	5191	2	CQ861643	CQ861643 Sequence
32	1234	75.8	5191	2	AX335501	AX335501 Sequence
33	1234	75.8	5191	2	AX774776	AX774776 Sequence
34	1234	75.8	5191	5	HUMIL8A	M28130 Human inter
35	1198.6	73.6	172536	12	AC136879	AC136879 Pan trogl
36	639.2	39.2	645	2	AX256012	AX256012 Sequence
37	619.8	38.0	660	2	CQ820022	CQ820022 Sequence
38	619.8	38.0	660	2	CQ820024	CQ820024 Sequence
39	588.6	36.1	601	7	BV167919	BV167919 sqnm6819
40	582.2	35.7	1500	14	RABNAP1	M57439 Rabbit neut
41	569.2	34.9	712	7	BV680182	BV680182 IL8_V108
42	568.2	34.9	619	2	BD229536	BD229536 Human gen
43	568.2	34.9	619	2	CQ973490	CQ973490 Sequence
44	562.8	34.5	706	7	BV166388	BV166388 IL8_746 R
45	521.8	32.0	601	7	BV179378	BV179378 sqnm10508

ALIGNMENTS

RESULT 1
AR762925

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 05:02:23 ; Search time 911.634 Seconds
(without alignments)
12458.724 Million cell updates/sec

Title: US-10-690-880-1
Perfect score: 1629
Sequence: 1 gcagagcacacaagcttcta.....atataatttggtgtcaaagt 1629

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1629	100.0	1629	14	ADW72103	Adw72103 Human IL8
2	1594	97.9	1633	6	AAD46736	Aad46736 Human int
3	1594	97.9	1666	11	ADN95506	Adn95506 Human BEC
4	1594	97.9	1666	12	ADH17183	Adh17183 Human IL-
5	1594	97.9	1666	12	ADN12149	Adn12149 Interleuk
6	1594	97.9	1666	12	ADP10398	Adp10398 Reference
7	1594	97.9	1666	12	ADQ09327	Adq09327 Human IL8
8	1594	97.9	1666	14	ADY19491	Ady19491 DNA encod
9	1594	97.9	1666	14	ADY14931	Ady14931 DNA encod
10	1594	97.9	1666	14	ADZ26524	Adz26524 Human IL8
11	1594	97.9	1666	14	AEA04360	Aea04360 Human cDN
12	1594	97.9	1666	14	AEB54686	Aeb54686 DNA encod
13	1594	97.9	1666	14	AEC75887	Aec75887 Genetic m
14	1594	97.9	1666	15	AEF92714	Aef92714 Human int
15	1584.8	97.3	1708	8	ABX63815	Abx63815 Human cDN
16	1584.8	97.3	1708	9	ADA11056	Ada11056 Human cDN
17	1584.8	97.3	1708	12	ADG47966	Adg47966 Human IL-
18	1580.4	97.0	1639	2	AAQ74059	Aaq74059 Human int
19	1580.4	97.0	1639	2	AAX14999	Aax14999 DNA encod
20	1580.4	97.0	1639	6	ABZ35158	Abz35158 Human gen
21	1580.4	97.0	1639	6	ABK83942	Abk83942 Human cDN
22	1580.4	97.0	1639	8	ACC68893	Acc68893 Human int
23	1580.4	97.0	1639	8	ACA06054	Aca06054 Human CXC
24	1580.4	97.0	1639	9	ACD13645	Acd13645 DNA encod
25	1580.4	97.0	1639	10	ADE84956	Ade84956 Farnesyl
26	1580.4	97.0	1639	10	ADH28980	Adh28980 Human chr
27	1580.4	97.0	1639	10	ADK61280	Adk61280 Ovarian c
28	1580.4	97.0	1639	11	ADN95508	Adn95508 Human BEC
29	1580.4	97.0	1639	12	ADQ76209	Adq76209 Chemokine
30	1580.4	97.0	1639	14	AEA49857	Aea49857 Human che
31	1569.4	96.3	1639	4	AAH02920	Aah02920 Human she
32	1569.4	96.3	1639	6	ABZ35194	Abz35194 Human gen
33	1569.4	96.3	1639	6	ABV77999	Abv77999 Hypoxia-r
34	1569.4	96.3	1639	8	ACC50984	Acc50984 Human bla
35	1569.4	96.3	1639	8	ACF12874	Acf12874 Human cer
36	1569.4	96.3	1639	11	ADN38868	Adn38868 Cancer/an
37	1569.4	96.3	1639	11	ADN39674	Adn39674 Cancer/an
38	1569.4	96.3	1639	12	ADN01989	Adn01989 Human inf
39	1569.4	96.3	1639	12	ADN05784	Adn05784 Antipsori
40	1569.4	96.3	1639	12	ADO24406	Ado24406 Human PRO
41	1569.4	96.3	1639	12	ADO24378	Ado24378 Human PRO
42	1569.4	96.3	1639	12	ADQ29581	Adq29581 Human col
43	1569.4	96.3	1639	13	ADR24636	Adr24636 Breast ca
44	1569.4	96.3	1639	13	ADR24535	Adr24535 Breast ca
45	1569.4	96.3	1639	13	ADP54385	Adp54385 Human PRO

ALIGNMENTS

RESULT 1
ADW72103

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-1.

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This page gives you Search Results detail for the Application 10690880 and Search Result us-10-690-880-1.rni.

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 05:55:31 ; Search time 297.039 Seconds
(without alignments)
10261.408 Million cell updates/sec

Title: US-10-690-880-1
Perfect score: 1629
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
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- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1480.8	90.9	1560	3	US-08-818-631A-1	Sequence 1, Appli
6	1480.8	90.9	1560	3	US-10-037-218A-1	Sequence 1, Appli
7	1480.8	90.9	1560	3	US-09-016-434-1340	Sequence 1340, Ap
8	1480.8	90.9	1560	3	US-09-220-132-75	Sequence 75, Appl
9	1480.8	90.9	1560	4	US-08-927-939A-58	Sequence 58, Appl
10	1480.8	90.9	1560	5	US-09-543-679A-2598	Sequence 2598, Ap
c 11	1260	77.3	1512	5	US-09-984-429-574	Sequence 574, App
12	1234	75.8	5191	5	US-09-543-679A-2556	Sequence 2556, Ap
13	568.2	34.9	619	3	US-09-385-982-211	Sequence 211, App
14	281.8	17.3	297	10	5451399-1	Patent No. 5451399
15	205.4	12.6	219	2	US-08-330-163-36	Sequence 36, Appl
16	205.4	12.6	219	2	US-08-482-111-36	Sequence 36, Appl
17	195.2	12.0	365	3	US-09-046-894-2	Sequence 2, Appli
18	191.2	11.7	229	2	US-08-482-111-50	Sequence 50, Appl
19	191	11.7	228	2	US-08-482-111-52	Sequence 52, Appl
20	191	11.7	257	3	US-09-016-434-769	Sequence 769, App
21	189.4	11.6	219	2	US-08-330-163-41	Sequence 41, Appl
22	189.4	11.6	219	2	US-08-482-111-41	Sequence 41, Appl
23	188.6	11.6	231	2	US-08-482-111-56	Sequence 56, Appl
24	185.4	11.4	241	2	US-08-143-576-14	Sequence 14, Appl
25	185.4	11.4	241	3	US-09-221-268D-19	Sequence 19, Appl
26	179.2	11.0	228	2	US-08-482-111-54	Sequence 54, Appl
c 27	172.2	10.6	402	3	US-10-131-827-8532	Sequence 8532, Ap
c 28	172.2	10.6	402	5	US-10-131-831-8532	Sequence 8532, Ap
29	161.4	9.9	578	3	US-10-131-827-8568	Sequence 8568, Ap
30	161.4	9.9	578	5	US-10-131-831-8568	Sequence 8568, Ap
31	139	8.5	182	3	US-09-513-999C-8394	Sequence 8394, Ap
32	121	7.4	598	3	US-09-046-894-3	Sequence 3, Appli
c 33	99.6	6.1	244	5	US-09-543-679A-1791	Sequence 1791, Ap
c 34	99.6	6.1	7033	5	US-09-543-679A-2411	Sequence 2411, Ap
c 35	99.6	6.1	209274	5	US-09-543-679A-3004	Sequence 3004, Ap
36	90	5.5	1182	3	US-09-811-162-1	Sequence 1, Appli
c 37	87	5.3	99	2	US-08-330-163-38	Sequence 38, Appl
38	87	5.3	99	2	US-08-330-163-39	Sequence 39, Appl
c 39	87	5.3	99	2	US-08-482-111-38	Sequence 38, Appl
40	87	5.3	99	2	US-08-482-111-39	Sequence 39, Appl
41	79.8	4.9	139	2	US-08-086-410-31	Sequence 31, Appl
42	74.6	4.6	41100	3	US-09-755-665-46	Sequence 46, Appl
43	74	4.5	1141	3	US-09-806-708B-22	Sequence 22, Appl
44	70.8	4.3	451924	3	US-09-949-016-12896	Sequence 12896, A
45	70.8	4.3	451925	3	US-09-949-016-17305	Sequence 17305, A

ALIGNMENTS

RESULT 1

US-09-811-162-3

; Sequence 3, Application US/09811162

; Patent No. 6962971

; GENERAL INFORMATION:

; APPLICANT: Martins-Green, Manuela

; APPLICANT: Feugate, Jo Ellen

; APPLICANT: Li, QiJing

; TITLE OF INVENTION: Chemokines and Methods for Inducing the Differentiation of Fibr

; TITLE OF INVENTION: Myofibroblasts

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-1.rn

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 06:23:19 ; Search time 1813.47 Seconds
(without alignments)
11037.706 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

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5	1594	97.9	1666	9	US-10-278-698-4	Sequence 4, Appli
6	1594	97.9	1666	9	US-10-278-698-1043	Sequence 1043, Ap
7	1594	97.9	1666	16	US-11-179-848-247	Sequence 247, App
8	1584.8	97.3	1708	3	US-09-981-353-174	Sequence 174, App
9	1584.8	97.3	1708	6	US-10-044-090-815	Sequence 815, App
10	1584.8	97.3	1708	6	US-10-235-994-5	Sequence 5, Appli
11	1580.4	97.0	1639	3	US-09-960-143-3	Sequence 3, Appli
12	1580.4	97.0	1639	6	US-10-104-755-77	Sequence 77, Appl
13	1580.4	97.0	1639	6	US-10-171-581-248	Sequence 248, App
14	1580.4	97.0	1639	7	US-10-101-510-270	Sequence 270, App
15	1580.4	97.0	1639	8	US-10-240-425-1298	Sequence 1298, Ap
16	1580.4	97.0	1639	8	US-10-283-975A-175	Sequence 175, App
17	1580.4	97.0	1639	10	US-10-505-680-450	Sequence 450, App
18	1580.4	97.0	1639	10	US-10-970-698A-13	Sequence 13, Appl
19	1569.4	96.3	1639	6	US-10-171-311-92	Sequence 92, Appl
20	1569.4	96.3	1639	7	US-10-101-510-306	Sequence 306, App
21	1569.4	96.3	1639	7	US-10-301-822-86	Sequence 86, Appl
22	1569.4	96.3	1639	7	US-10-170-385-252	Sequence 252, App
23	1569.4	96.3	1639	7	US-10-172-118-396	Sequence 396, App
24	1569.4	96.3	1639	7	US-10-172-118-497	Sequence 497, App
25	1569.4	96.3	1639	7	US-10-295-027-186	Sequence 186, App
26	1569.4	96.3	1639	7	US-10-295-027-992	Sequence 992, App
27	1569.4	96.3	1639	8	US-10-342-887-396	Sequence 396, App
28	1569.4	96.3	1639	8	US-10-342-887-497	Sequence 497, App
29	1569.4	96.3	1639	8	US-10-188-832-61	Sequence 61, Appl
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31	1569.4	96.3	1639	8	US-10-734-564-7	Sequence 7, Appli
32	1569.4	96.3	1639	15	US-11-186-284-86	Sequence 86, Appl
33	1569.4	96.3	1639	16	US-11-091-883-4	Sequence 4, Appli
34	1561	95.8	1605	10	US-10-929-182-20	Sequence 20, Appl
35	1517.4	93.1	2206	3	US-09-971-392-249	Sequence 249, App
36	1516	93.1	3154	3	US-09-981-353-176	Sequence 176, App
37	1516	93.1	3154	6	US-10-071-766-131	Sequence 131, App
38	1491.4	91.6	1791	6	US-10-198-846-13844	Sequence 13844, A
39	1480.8	90.9	1560	2	US-08-927-939-58	Sequence 58, Appl
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42	1480.8	90.9	1560	9	US-10-723-860-207	Sequence 207, App
43	1480.8	90.9	1560	10	US-10-831-704-75	Sequence 75, Appl
44	1480.8	90.9	1560	12	US-10-241-375-58	Sequence 58, Appl
45	1479.2	90.8	1560	6	US-10-121-119-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-690-880-1

; Sequence 1, Application US/10690880

; Publication No. US20050014165A1

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-1.rnpbn.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions
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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 06:25:38 ; Search time 186.874 Seconds
(without alignments)
12153.869 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 5	1550.4	95.2	1596	8	US-11-266-748A-19603	Sequence 19603, A
6	1550.4	95.2	1596	8	US-11-266-748A-62371	Sequence 62371, A
c 7	1550.4	95.2	1596	8	US-11-266-748A-65210	Sequence 65210, A
8	985	60.5	1000	8	US-11-266-748A-283835	Sequence 283835,
c 9	985	60.5	1000	8	US-11-266-748A-335264	Sequence 335264,
10	985	60.5	1000	8	US-11-266-748A-393627	Sequence 393627,
c 11	985	60.5	1000	8	US-11-266-748A-464673	Sequence 464673,
12	948.2	58.2	963	8	US-11-266-748A-216339	Sequence 216339,
13	576.2	35.4	849	8	US-11-266-748A-184571	Sequence 184571,
14	565	34.7	574	8	US-11-266-748A-15238	Sequence 15238, A
15	511	31.4	550	8	US-11-266-748A-218857	Sequence 218857,
c 16	384.8	23.6	609	8	US-11-266-748A-33252	Sequence 33252, A
17	72	4.4	5286	6	US-10-517-441-294	Sequence 294, App
18	72	4.4	5286	6	US-10-517-441-568	Sequence 568, App
19	72	4.4	8900	6	US-10-517-441-701	Sequence 701, App
20	70.4	4.3	8900	6	US-10-517-441-427	Sequence 427, App
c 21	68.4	4.2	1086	8	US-11-217-529-166166	Sequence 166166,
c 22	68.2	4.2	5286	6	US-10-517-441-294	Sequence 294, App
c 23	68.2	4.2	5286	6	US-10-517-441-568	Sequence 568, App
24	66.6	4.1	3647	6	US-10-517-441-373	Sequence 373, App
25	66.6	4.1	3647	6	US-10-517-441-647	Sequence 647, App
26	65.6	4.0	4001	6	US-10-517-441-509	Sequence 509, App
27	65.6	4.0	4001	6	US-10-517-441-783	Sequence 783, App
28	65	4.0	5286	6	US-10-517-441-293	Sequence 293, App
c 29	65	4.0	5286	6	US-10-517-441-293	Sequence 293, App
30	65	4.0	5286	6	US-10-517-441-567	Sequence 567, App
c 31	65	4.0	5286	6	US-10-517-441-567	Sequence 567, App
32	65	4.0	6343	6	US-10-517-441-412	Sequence 412, App
33	64.8	4.0	9001	6	US-10-517-441-789	Sequence 789, App
34	64.2	3.9	1000	8	US-11-266-748A-281979	Sequence 281979,
c 35	64.2	3.9	1000	8	US-11-266-748A-308619	Sequence 308619,
36	63.8	3.9	170452	8	US-11-266-748A-23170	Sequence 23170, A
37	63.4	3.9	6343	6	US-10-517-441-686	Sequence 686, App
38	63	3.9	8759	6	US-10-517-441-256	Sequence 256, App
39	63	3.9	8759	6	US-10-517-441-530	Sequence 530, App
40	62.8	3.9	340000	8	US-11-266-748A-61353	Sequence 61353, A
41	62.4	3.8	16579	6	US-10-517-441-289	Sequence 289, App
42	62.4	3.8	16579	6	US-10-517-441-563	Sequence 563, App
43	62	3.8	16579	6	US-10-517-441-564	Sequence 564, App
c 44	61.6	3.8	3647	6	US-10-517-441-374	Sequence 374, App
c 45	61.6	3.8	3647	6	US-10-517-441-648	Sequence 648, App

ALIGNMENTS

RESULT 1

US-11-242-111-1

; Sequence 1, Application US/11242111

; Publication No. US20060088862A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Nancy M

; TITLE OF INVENTION: DRUG SCREENING AND MOLECULAR DIAGNOSTIC TEST FOR EARLY DETECTIO

; TITLE OF INVENTION: OF COLORECTAL CANCER: REAGENTS, METHODS, AND KITS THEREOF

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1565	96.1	1605	6	CR619554	CR619554 full-leng
5	1562	95.9	1597	6	CR623683	CR623683 full-leng
6	1559	95.7	1599	6	CR603686	CR603686 full-leng
7	1548	95.0	1577	6	CR600500	CR600500 full-leng
8	1533	94.1	1562	6	CR601533	CR601533 full-leng
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13	974	59.8	1134	4	BX398114	BX398114 BX398114
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19	915.8	56.2	960	4	BX360446	BX360446 BX360446
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21	904.4	55.5	1076	4	BX335640	BX335640 BX335640
22	882.2	54.2	1012	4	BX358167	BX358167 BX358167
c 23	862.8	53.0	1087	4	BX382446	BX382446 BX382446
c 24	859.4	52.8	1077	4	BX397622	BX397622 BX397622
25	851.8	52.3	921	4	BX453256	BX453256 BX453256
26	848.2	52.1	959	3	BQ934851	BQ934851 AGENCOURT
27	842.2	51.7	1005	3	BM924085	BM924085 AGENCOURT
28	834.4	51.2	1014	4	BX462017	BX462017 BX462017
29	829.4	50.9	896	4	BX429908	BX429908 BX429908
c 30	821.6	50.4	871	4	BX413857	BX413857 BX413857
31	806.4	49.5	989	3	BM907331	BM907331 AGENCOURT
32	803.2	49.3	854	3	BQ431044	BQ431044 AGENCOURT
33	795.2	48.8	867	3	BQ232784	BQ232784 AGENCOURT
34	792.6	48.7	1000	3	BQ225540	BQ225540 AGENCOURT
35	787.2	48.3	1015	3	BM924065	BM924065 AGENCOURT
36	786.4	48.3	867	3	BQ932618	BQ932618 AGENCOURT
37	784.2	48.1	924	3	BU928951	BU928951 AGENCOURT
38	763.8	46.9	882	3	BQ231178	BQ231178 AGENCOURT
39	758.6	46.6	899	3	BU186293	BU186293 AGENCOURT
40	757.6	46.5	958	3	BM907296	BM907296 AGENCOURT
41	737.4	45.3	846	3	BU153304	BU153304 AGENCOURT
42	737.2	45.3	831	3	BQ215118	BQ215118 AGENCOURT
43	734	45.1	986	8	CO646425	CO646425 ILLUMIGEN
44	733.4	45.0	772	4	BX337862	BX337862 BX337862
45	727.2	44.6	984	8	CO648285	CO648285 ILLUMIGEN

ALIGNMENTS

RESULT 1

CR601902

LOCUS CR601902 1620 bp mRNA linear HTC 21-JUL-2004

Comments /
Suggestions

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	1821.2	98.4	1854	2	AX774792	AX774792 Sequence
6	1821.2	98.4	1854	5	HUMPPAR	L02932 Human perox
7	1731	93.6	1731	2	AX522244	AX522244 Sequence
8	1731	93.6	1731	5	S74349	S74349 hPPAR alpha
9	1554	84.0	1566	5	CR456547	CR456547 Homo sapi
10	1403.8	75.9	1407	5	CR457435	CR457435 Homo sapi
11	1400.6	75.7	1407	5	HSPPARAGE	Y07619 H.sapiens m
12	1394.2	75.4	1407	2	I73722	I73722 Sequence 1
13	1349	72.9	1383	2	CQ730484	CQ730484 Sequence
14	1333.4	72.1	1404	5	DQ062812	DQ062812 Macaca mu
15	1185.2	64.1	2032	2	BD171828	BD171828 Canine pr
16	1185.2	64.1	2032	14	AF350327	AF350327 Canis fam
17	1109.6	60.0	1979	14	BT020756	BT020756 Bos tauru
18	1092.2	59.0	1411	14	AF229356	AF229356 Bos tauru
19	1090.2	58.9	2336	6	BC016892	BC016892 Mus muscu
20	1085.4	58.7	2081	2	AR477503	AR477503 Sequence
21	1085.4	58.7	2081	6	MMPPAR	X57638 Mouse mRNA
22	1080.6	58.4	1407	6	MAU555631	AJ555631 Mesocrice
23	1078.2	58.3	2022	6	RATPPAR	M88592 Rattus ratt
24	1064.4	57.5	1404	14	AF228696	AF228696 Sus scrof
25	980.8	53.0	2073	6	CPAJ222	AJ000222 Cavia por
26	955.4	51.6	1610	6	CPO6218	AJ006218 Cavia por
27	944	51.0	2100	11	AF163809	AF163809 Gallus ga
28	944	51.0	2100	11	AF470455	AF470455 Gallus ga
29	935.2	50.6	1515	14	AF463455	AF463455 Phascolar
30	922	49.8	1455	11	AF481797	AF481797 Anser ans
31	806.6	43.6	3250	11	XELPPARA	M84161 Xenopus lae
32	805	43.5	3355	11	BC060004	BC060004 Xenopus l
33	805	43.5	3620	11	BC079684	BC079684 Xenopus l
34	784.8	42.4	4592	11	BC087622	BC087622 Xenopus l
35	740	40.0	1571	5	BC000052	BC000052 Homo sapi
36	683.2	36.9	984	11	CNI011515	AJ011515 Crocodylu
37	661.4	35.8	831	6	AY170844	AY170844 Mesocrice
38	648.8	35.1	867	2	AX522246	AX522246 Sequence
39	588.2	31.8	1326	5	AY919140	AY919140 Homo sapi
40	588.2	31.8	1505	2	CQ716556	CQ716556 Sequence
41	586.6	31.7	1792	2	AR448302	AR448302 Sequence
42	586.6	31.7	2961	2	AX522248	AX522248 Sequence
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ALIGNMENTS

RESULT 1
CS177463

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-15.rni.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10690880 and Search Result us-10-690-880-15.rni.

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 05:55:31 ; Search time 337.337 Seconds
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5	1085.4	58.7	2081	3	US-10-329-668-11	Sequence 11, Appl
6	588.2	31.8	1505	3	US-09-949-016-5726	Sequence 5726, Ap
7	586.6	31.7	1792	3	US-09-976-594-999	Sequence 999, App
8	586.6	31.7	3301	3	US-09-166-265-8	Sequence 8, Appli
9	570.2	30.8	2009	2	US-08-333-358-9	Sequence 9, Appli
10	570.2	30.8	2009	2	US-08-463-694-9	Sequence 9, Appli
11	570.2	30.8	2009	2	US-08-694-501-9	Sequence 9, Appli
12	565.2	30.6	2012	2	US-08-484-200-3	Sequence 3, Appli
13	564.2	30.5	1323	3	US-10-329-668-13	Sequence 13, Appl
14	485.2	26.2	1434	3	US-09-128-142-1	Sequence 1, Appli
15	485.2	26.2	1518	3	US-09-128-142-3	Sequence 3, Appli
16	485.2	26.2	1518	3	US-09-016-434-1136	Sequence 1136, Ap
17	485.2	26.2	1608	3	US-09-484-345-3	Sequence 3, Appli
18	485.2	26.2	1608	3	US-09-765-111A-15	Sequence 15, Appl
19	485.2	26.2	1812	3	US-09-949-016-3749	Sequence 3749, Ap
20	485.2	26.2	1812	3	US-09-949-016-3750	Sequence 3750, Ap
21	485.2	26.2	1841	3	US-09-587-549C-1	Sequence 1, Appli
22	485.2	26.2	2334	3	US-09-765-111A-1	Sequence 1, Appli
23	485.2	26.2	2523	3	US-09-765-111A-3	Sequence 3, Appli
24	485.2	26.2	2596	3	US-09-765-111A-22	Sequence 22, Appl
25	485.2	26.2	2625	3	US-09-765-111A-5	Sequence 5, Appli
26	475.6	25.7	1811	3	US-09-166-265-6	Sequence 6, Appli
27	475.6	25.7	1811	3	US-09-765-111A-26	Sequence 26, Appl
28	475.6	25.7	1811	4	US-09-880-107-2212	Sequence 2212, Ap
29	475.6	25.7	1844	3	US-08-134-557D-1	Sequence 1, Appli
30	474.4	25.6	1796	3	US-09-255-392-1	Sequence 1, Appli
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33	474.4	25.6	2005	3	US-08-465-375-1	Sequence 1, Appli
34	474.4	25.6	2005	3	US-09-788-070-1	Sequence 1, Appli
35	474.4	25.6	2005	3	US-10-142-373-1	Sequence 1, Appli
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38	471.6	25.5	87752	3	US-09-949-016-16807	Sequence 16807, A
39	339	18.3	601	3	US-09-949-016-177428	Sequence 177428,
40	242.6	13.1	88906	3	US-09-949-016-17468	Sequence 17468, A
41	215	11.6	601	3	US-09-949-016-177427	Sequence 177427,
42	196.8	10.6	86877	3	US-09-949-016-15491	Sequence 15491, A
43	196.8	10.6	86877	3	US-09-949-016-15492	Sequence 15492, A
44	97	5.2	2067	3	US-09-106-194-11	Sequence 11, Appl
45	90.8	4.9	601	3	US-09-949-016-177396	Sequence 177396,

ALIGNMENTS

RESULT 1

US-09-662-386-1

; Sequence 1, Application US/09662386

; Patent No. 6544743

; GENERAL INFORMATION:

; APPLICANT: Hudson, Thomas J.

; APPLICANT: Vohl, Marie-Claude

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-15.rnpbm.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1432	77.4	1646	8	US-10-317-500-276	Sequence 276, App
7	1407	76.1	1407	7	US-10-414-692-1	Sequence 1, Appli
8	1407	76.1	1407	10	US-10-502-279-5	Sequence 5, Appli
9	1085.4	58.7	2081	7	US-10-327-813-11	Sequence 11, Appl
10	1085.4	58.7	2081	7	US-10-329-668-11	Sequence 11, Appl
11	1085.4	58.7	2081	8	US-10-317-500-11	Sequence 11, Appl
12	1085.4	58.7	2081	9	US-10-717-049-11	Sequence 11, Appl
13	1085.4	58.7	2081	10	US-10-899-458-23	Sequence 23, Appl
14	1084.2	58.6	1897	8	US-10-317-500-107	Sequence 107, App
15	1075	58.1	2150	16	US-11-136-527-2287	Sequence 2287, Ap
16	740	40.0	1580	8	US-10-317-500-20	Sequence 20, Appl
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19	600	32.4	600	13	US-11-060-756-2516	Sequence 2516, Ap
20	600	32.4	600	13	US-11-060-756-6787	Sequence 6787, Ap
21	600	32.4	600	13	US-11-060-756-6788	Sequence 6788, Ap
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26	586.6	31.7	3301	8	US-10-655-847-18	Sequence 18, Appl
27	586.6	31.7	3301	8	US-10-717-597-17	Sequence 17, Appl
28	586.6	31.7	3301	9	US-10-690-880-17	Sequence 17, Appl
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35	564.2	30.5	1323	7	US-10-329-668-13	Sequence 13, Appl
36	564.2	30.5	1323	7	US-10-160-807-99	Sequence 99, Appl
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38	564.2	30.5	1323	9	US-10-717-049-13	Sequence 13, Appl
39	564.2	30.5	1323	10	US-10-899-458-25	Sequence 25, Appl
40	560.8	30.3	2175	16	US-11-136-527-2262	Sequence 2262, Ap
41	501.2	27.1	1636	10	US-10-764-420-103	Sequence 103, App
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ALIGNMENTS

RESULT 1

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Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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SUMMARIES

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5	1656	89.5	8497	8	US-11-266-748A-29152	Sequence 29152, A
6	1656	89.5	8497	8	US-11-266-748A-56572	Sequence 56572, A
7	815.2	44.1	1014	8	US-11-289-656-1	Sequence 1, Appli
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15	485.2	26.2	1734	8	US-11-283-329-21	Sequence 21, Appl
16	485.2	26.2	1735	6	US-10-505-928-143	Sequence 143, App
17	485.2	26.2	1767	8	US-11-145-307A-165	Sequence 165, App
18	485.2	26.2	1767	8	US-11-283-329-25	Sequence 25, Appl
19	485.2	26.2	1808	8	US-11-266-748A-28881	Sequence 28881, A
20	485.2	26.2	1836	8	US-11-283-329-27	Sequence 27, Appl
21	485.2	26.2	1854	8	US-11-283-329-23	Sequence 23, Appl
22	485.2	26.2	1863	8	US-11-289-781-3	Sequence 3, Appli
23	471.6	25.5	86215	8	US-11-266-748A-24937	Sequence 24937, A
24	462	25.0	588	8	US-11-266-748A-13140	Sequence 13140, A
25	457.4	24.7	1977	8	US-11-266-748A-25551	Sequence 25551, A
26	455.8	24.6	1977	8	US-11-283-329-19	Sequence 19, Appl
27	452.8	24.5	609	8	US-11-266-748A-217434	Sequence 217434,
c 28	452.8	24.5	609	8	US-11-266-748A-238624	Sequence 238624,
29	430.4	23.3	1089	8	US-11-289-656-9	Sequence 9, Appli
30	430.4	23.3	1089	8	US-11-289-781-16	Sequence 16, Appl
31	356.2	19.3	1455	8	US-11-266-748A-94271	Sequence 94271, A
c 32	356.2	19.3	1455	8	US-11-266-748A-147082	Sequence 147082,
33	349.4	18.9	1017	8	US-11-289-656-5	Sequence 5, Appli
34	349.4	18.9	1017	8	US-11-289-781-12	Sequence 12, Appl
35	338.4	18.3	1000	8	US-11-266-748A-292279	Sequence 292279,
c 36	338.4	18.3	1000	8	US-11-266-748A-343708	Sequence 343708,
37	338.4	18.3	1000	8	US-11-266-748A-403930	Sequence 403930,
c 38	338.4	18.3	1000	8	US-11-266-748A-474976	Sequence 474976,
39	334.4	18.1	1000	8	US-11-266-748A-286681	Sequence 286681,
c 40	334.4	18.1	1000	8	US-11-266-748A-338110	Sequence 338110,
c 41	329.8	17.8	950	8	US-11-266-748A-215920	Sequence 215920,
42	329.8	17.8	950	8	US-11-266-748A-237901	Sequence 237901,
43	208.4	11.3	1000	8	US-11-266-748A-293453	Sequence 293453,
c 44	208.4	11.3	1000	8	US-11-266-748A-344882	Sequence 344882,
45	208.4	11.3	1000	8	US-11-266-748A-405482	Sequence 405482,

ALIGNMENTS

RESULT 1

US-11-242-111-11

; Sequence 11, Application US/11242111

; Publication No. US20060088862A1

GENERAL INFORMATION:

; APPLICANT: Lee, Nancy M

; TITLE OF INVENTION: DRUG SCREENING AND MOLECULAR DIAGNOSTIC TEST FOR EARLY DETECTIO

; TITLE OF INVENTION: OF COLORECTAL CANCER: REAGENTS, METHODS, AND KITS THEREOF

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-15.rng.

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Suggestions

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OM nucleic - nucleic search, using sw model

```
Run on:      July 13, 2006, 05:02:23 ; Search time 1035.31 Seconds
              (without alignments)
              12458.724 Million cell updates/sec
```

Title: US-10-690-880-15
Perfect score: 1850
Sequence: 1 ggcccaggctgaagctcagg.....ctaattctcaggactgggaag 1850

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      N_Geneseq_8:*
1:  geneseqn1980s:*
2:  geneseqn1990s:*
3:  geneseqn2000s:*
4:  geneseqn2001as:*
5:  geneseqn2001bs:*
6:  geneseqn2002as:*
7:  geneseqn2002bs:*
8:  geneseqn2003as:*
9:  geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1850	100.0	1850	4	AAF30517	Aaf30517 Peroxisom
2	1850	100.0	1850	12	ADP68582	Adp68582 Human PPA
3	1850	100.0	1850	13	ACN40971	Acn40971 Tumour-as
4	1850	100.0	1850	14	ADW72117	Adw72117 Human PPA
5	1850	100.0	1850	14	AED14714	Aed14714 Human per
6	1821.2	98.4	1854	2	AAX36521	Aax36521 Human PPA
7	1821.2	98.4	1854	10	ADE84889	Ade84889 Farnesyl
8	1821.2	98.4	1854	15	AEF50937	Aef50937 Human PPA
9	1731	93.6	1731	6	ABS52758	Abs52758 Human per
10	1432	77.4	1646	12	ADP68840	Adp68840 Human PPA
11	1407	76.1	1407	2	AAQ92081	Aaq92081 Human per
12	1407	76.1	1407	10	ADB80260	Adb80260 PPARgamma
13	1407	76.1	1407	12	ADJ92802	Adj92802 Human per
14	1407	76.1	1407	12	ADP05746	Adp05746 Human nuc
15	1404	75.9	1404	12	ADI05806	Adi05806 Human per
16	1309	70.8	3292	13	ACN43039	Acn43039 Human dia
17	1278.2	69.1	3644	13	ACN43038	Acn43038 Human dia
18	1277	69.0	1497	10	ADI21861	Adi21861 Novel hum
19	1185.2	64.1	2032	6	AAL41440	Aal41440 2032nt do
20	1085.4	58.7	2081	9	ACF36092	Acf36092 Human PPA
21	1085.4	58.7	2081	9	ACF04418	Acf04418 Human PPA
22	1085.4	58.7	2081	12	ADP05748	Adp05748 Mouse nuc
23	1085.4	58.7	2081	12	ADP68575	Adp68575 Mouse PPA
24	1084.2	58.6	1897	12	ADP68671	Adp68671 Mouse PPA
25	1019.2	55.1	1024	10	ABZ83257	Abz83257 Toxicolog
26	740	40.0	1580	12	ADP68584	Adp68584 Human PPA
27	648.8	35.1	867	6	ABS52759	Abs52759 Human PPA
28	586.6	31.7	1326	2	AAT10583	Aat10583 Peroxisom
29	586.6	31.7	1326	12	ADJ92803	Adj92803 Human per
30	586.6	31.7	1326	12	ADP05754	Adp05754 Human nuc
31	586.6	31.7	1326	14	ADV43463	Adv43463 Human psy
32	586.6	31.7	1792	12	ADL13270	Adl13270 Human ste
33	586.6	31.7	2961	6	ABS52760	Abs52760 Human per
34	586.6	31.7	3294	2	AAQ48939	Aaq48939 Steroid h
35	586.6	31.7	3301	2	AAX36523	Aax36523 Human PPA
36	586.6	31.7	3301	6	ABL65244	Abl65244 Lung canc
37	586.6	31.7	3301	12	ADG86782	Adg86782 Human per
38	586.6	31.7	3301	12	ADL34720	Adl34720 Human PPA
39	586.6	31.7	3301	12	ADN03625	Adn03625 Antipsori
40	586.6	31.7	3301	12	ADP13281	Adp13281 Renal cel
41	586.6	31.7	3301	13	ADP22937	Adp22937 PRO polyp
42	586.6	31.7	3301	14	ADW72119	Adw72119 Human PPA
43	586.6	31.7	3301	14	AED07739	Aed07739 Human per
44	586.6	31.7	3301	15	AEF50939	Aef50939 Human PPA
45	586.6	31.7	3302	12	ADQ83749	Adq83749 Human tum

ALIGNMENTS

RESULT 1
AAF30517

SCORE Search Results Details for Application 10690880 and Search Result us-10-690-880-15.rst.

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OM nucleic - nucleic search, using sw model

Run on: July 13, 2006, 05:54:59 ; Search time 9099.91 Seconds
(without alignments)
11368.329 Million cell updates/sec

Title: US-10-690-880-15
Perfect score: 1850
Sequence: 1 ggcccaggctgaagctcagg.....ctaattctcaggactgggaag 1850

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	1407	76.1	1407	14	AY421083	AY421083 Homo sapi
	2	1140.4	61.6	1159	14	AY421084	AY421084 Pan trogl
	3	1088.6	58.8	2026	6	AK149460	AK149460 Mus muscu
	4	1088.6	58.8	2519	6	AK081709	AK081709 Mus muscu
	5	1088.6	58.8	3413	6	AK035676	AK035676 Mus muscu
	6	1082.2	58.5	1407	14	AY421085	AY421085 Mus muscu
	7	740.2	40.0	876	8	CR979688	CR979688 CR979688
	8	717.4	38.8	920	3	BQ924716	BQ924716 AGENCOURT
	9	714.8	38.6	938	7	BE300333	BE300333 600944750
	10	684	37.0	815	7	BE300340	BE300340 600944783
	11	615.6	33.3	905	10	DV923305	DV923305 LB02930.C
c	12	614.2	33.2	800	5	CF410178	CF410178 CH3#065_C
	13	602.2	32.6	727	2	BG828014	BG828014 602752061
	14	574.6	31.1	809	7	BF306594	BF306594 601888837
	15	570	30.8	795	5	CF410179	CF410179 CH3#065_C
	16	564	30.5	577	9	DA762522	DA762522 DA762522
	17	548.8	29.7	817	9	DN534199	DN534199 1367135 M
	18	547.8	29.6	571	8	CV025749	CV025749 3513 Full
	19	547.8	29.6	821	3	BU144046	BU144046 603228808
	20	537	29.0	693	9	DN280937	DN280937 1162085 M
	21	490	26.5	862	7	BB894707	BB894707 BB894707
	22	485.2	26.2	1402	6	CR609113	CR609113 full-leng
	23	485.2	26.2	1425	6	CR605352	CR605352 full-leng
	24	485.2	26.2	1518	14	AY413103	AY413103 Homo sapi
	25	485.2	26.2	1722	6	CR599329	CR599329 full-leng
	26	485.2	26.2	1740	6	CR609454	CR609454 full-leng
	27	485.2	26.2	1828	6	CR857213	CR857213 Pongo pyg
	28	484.8	26.2	960	10	DV768426	DV768426 ILLUMIGEN
	29	483.6	26.1	1518	14	AY413104	AY413104 Pan trogl
	30	474.4	25.6	1518	14	AY413105	AY413105 Mus muscu
c	31	473.6	25.6	566	1	AI739497	AI739497 wi14c08.x
c	32	468.8	25.3	558	1	AI739498	AI739498 wi14c09.x
	33	467.8	25.3	692	3	BU306743	BU306743 603609553
c	34	467	25.2	547	1	AI768604	AI768604 wh23h06.x
	35	466.6	25.2	737	5	CF521623	CF521623 AGENCOURT
	36	464.2	25.1	1866	6	CR622226	CR622226 full-leng
	37	457	24.7	1078	14	DQ035710	DQ035710 Homo sapi
	38	453.8	24.5	692	3	BU245821	BU245821 603784005
	39	452.8	24.5	609	3	BP238961	BP238961 BP238961
	40	451.2	24.4	1740	6	AK089913	AK089913 Mus muscu
	41	450.6	24.4	1078	14	DQ035711	DQ035711 Pan trogl
c	42	434.8	23.5	535	1	AI380344	AI380344 tf94h12.x
c	43	425.6	23.0	484	1	AI761514	AI761514 wi61c09.x
	44	424	22.9	547	7	BE168040	BE168040 QV3-HT051
	45	421	22.8	470	3	BU585012	BU585012 7936927H1

ALIGNMENTS

RESULT 1

AY421083

LOCUS AY421083 1407 bp DNA linear GSS 12-DEC-2003